(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/132145

34,613

(B) FILING DATE: 12/9/96

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Guise, Jeffrey W.

(B) REGISTRATION NUMBER:

(C) REFERENCE/DOCKET NUMBER: 231/003

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (213) 489-1600

(B) TELEFAX: (213) 955-0440

(C) TELEX: 67-3510

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

786 base pairs

(B) TYPE:

nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY:

linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGATCGAAA	CATACAACCA	AACTTCTCCC	CGATCTGCGG	CCACTGGACT	GCCCATCAGC	60
ATGAAAATTT	TTATGTATTT	ACTTACTGTT	TTTCTTATCA	CCCAGATGAT	TGGGTCAGCA	120
CTTTTTGCTG	TGTATCTTCA	TAGAAGGTTG	GACAAGATAG	AAGATGAAAG	GAATCTTCAT	180
GAAGATTTTG	TATTCATGAA	AACGATACAG	AGATGCAACA	CAGGAGAAAG	ATCCTTATCC	240
TTACTGAACT	GTGAGGAGAT	TAAAAGCCAG	TTTGAAGGCT	TTGTGAAGGA	TATAATGTTA	300
AACAAAGAGG	AGACGAAGAA	AGAAAACAGC	TTTGAAATGC	AAAAAGGTGA	TCAGAATCCT	360
CAAATTGCGG	CACATGTCAT	AAGTGAGGCC	AGCAGTAAAA	CAACATCTGT	GTTACAGTGG	420
GCTGAAAAAG	GATACTACAC	CATGAGCAAC	AACTTGGTAA	CCCTGGAAAA	TGGGAAACAG	480
CTGACCGTTA	AAAGACAAGG	ACTCTATTAT	ATCTATGCCC	AAGTCACCTT	CTGTTCCAAT	540
CGGGAAGCTT	CGAGTCAAGC	TCCATTTATA	GCCAGCCTCT	GCCTAAAGTC	CCCCGGTAGA	600
TTCGAGAGAA	TCTTACTCAG	AGCTGCAAAT	ACCCACAGTT	CCGCCAAACC	TTGCGGGCAA	660
CAATCCATTC	ACTTGGGAGG	AGTATTTGAA	TTGCAACCAG	GTGCTTCGGT	GTTTGTCAAT	720
GTGACTGATC	CAAGCCAAGT	GAGCCATGGC	ACTGGCTTCA	CGTCCTTTGG	CTTACTCAAA	780
CTCTGA						786

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: single (D) TOPOLOGY:

linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGATAGAAA	CATACAGCCA	ACCTTCCCCC	AGATCCGTGG	CAACTGGACT	TCCAGCGAGC	60
ATGAAGATTT	TTATGTATTT	ACTTACTGTT	TTCCTTATCA	CCCAAATGAT	TGGATCTGTG	120
CTTTTTGCTG	TGTATCTTCA	TAGAAGATTG	GATAAGGTCG	AAGAGGAAGT	AAACCTTCAT	180
GAAGATTTTG	TATTCATAAA	AAAGCTAAAG	AGATGCAACA	AAGGAGAAGG	ATCTTTATCC	240
TTGCTGAACT	GTGAGGAGAT	GAGAAGGCAA	TTTGAAGACC	TTGTCAAGGA	TATAACGTTA	300
AACAAAGAAG	AGAAAAAAGA	AAACAGCTTT	GAAATGCAAA	GAGGTGATGA	GGATCCTCAA	360
ATTGCAGCAC	ACGTTGTAAG	CGAAGCCAAC	AGTAATGCAG	CATCCGTTCT	ACAGTGGGCC	420
AAGAAAGGAT	ATTATACCAT	GAAAAGCAAC	TTGGTAATGC	TTGAAAATGG	GAAACAGCTG	480
ACGGTTAAAA	GAGAAGGACT	CTATTATGTC	TACACTCAAG	TCACCTTCTG	CTCTAATCGG	540
GAGCCTTCGA	GTCAACGCCC	ATTCATCGTC	GGCCTCTGGC	TGAAGCCCAG	CATTGGATCT	600
GAGAGAATCT	TACTCAAGGC	GGCAAATACC	CACAGTTCCT	CCCAGCTTTG	CGAGCAGCAG	660
TCTGTTCACT	TGGGCGGAGT	GTTTGAATTA	CAAGCTGGTG	CTTCTGTGTT	TGTCAACGTG	720
ACTGAAGCAA	GCCAAGTGAT	CCACAGAGTT	GGCTTCTCAT	CTTTTGGCTT	ACTCAAACTC	780
TGA						783

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATGATCGAAA	CATACAACCA	AACTTCTCCC	CGATCTGCGG	CCACTGGACT	GCCCATCAGC	60
ATGAAAATTT	TTATGTATTT	ACTTACTGTT	TTTCTTATCA	CCCAGATGAT	TGGGTCAGCA	120
CTTTTTGCTG	TGTATCTTCA	TAGAAGATTG	GATAAGGTCG	AAGAGGAAGT	AAACCTTCAT	180
GAAGATTTTG	TATTCATAAA	AAAGCTAAAG	AGATGCAACA	AAGGAGAAGG	ATCTTTATCC	240
TTGCTGAACT	GTGAGGAGAT	GAGAAGGCAA	TTTGAAGACC	TTGTCAAGGA	TATAACGTTA	300
AACAAAGAAG	AGAAAAAAGA	AAACAGCTTT	GAAATGCAAA	GAGGTGATGA	GGATCCTCAA	360
ATTGCAGCAC	ACGTTGTAAG	CGAAGCCAAC	AGTAATGCAG	CATCCGTTCT	ACAGTGGGCC	420
AAGAAAGGAT	ATTATACCAT	GAAAAGCAAC	TTGGTAATGC	TTGAAAATGG	GAAACAGCTG	480
ACGGTTAAAA	GAGAAGGACT	CTATTATGTC	TACACTCAAG	TCACCTTCTG	CTCTAATCGG	540
GAGCCTTCGA	GTCAACGCCC	ATTCATCGTC	GGCCTCTGGC	TGAAGCCCAG	CATTGGATCT	600
GAGAGAATCT	TACTCAAGGC	GGCAAATACC	CACAGTTCCT	CCCAGCTTTG	CGAGCAGCAG	660
TCTGTTCACT	TGGGCGGAGT	GTTTGAATTA	CAAGCTGGTG	CTTCTGTGTT	TGTCAACGTG	720
ACTGAAGCAA	GCCAAGTGAT	CCACAGAGTT	GGCTTCTCAT	CTTTTGGCTT	ACTCAAACTC	780
TGA		•				783

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 786 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

> ma> > > mmm		3 COM 3 CO COM		~~~~		
ATGAAAATTT		ACTTACTGTT			TGGATCTGTG	120
CTTTTTGCTG	TGTATCTTCA	TAGAAGGTTG	GACAAGATAG	AAGATGAAAG	GAATCTTCAT	180
GAAGATTTTG	TATTCATGAA	AACGATACAG	AGATGCAACA	CAGGAGAAAG	ATCCTTATCC	240
TTACTGAACT	GTGAGGAGAT	TAAAAGCCAG	TTTGAAGGCT	TTGTGAAGGA	TATAATGTTA	300
AACAAAGAGG	AGACGAAGAA	AGAAAACAGC	TTTGAAATGC	AAAAAGGTGA	TCAGAATCCT	360
CAAATTGCGG	CACATGTCAT	AAGTGAGGCC	AGCAGTAAAA	CAACATCTGT	GTTACAGTGG	420
GCTGAAAAAG	GATACTACAC	CATGAGCAAC	AACTTGGTAA	CCCTGGAAAA	TGGGAAACAG	480
CTGACCGTTA	AAAGACAAGG	ACTCTATTAT	ATCTATGCCC	AAGTCACCTT	CTGTTCCAAT	540
CGGGAAGCTT	CGAGTCAAGC	TCCATTTATA	GCCAGCCTCT	GCCTAAAGTC	CCCCGGTAGA	600
TTCGAGAGAA	TCTTACTCAG	AGCTGCAAAT	ACCCACAGTT	CCGCCAAACC	TTGCGGGCAA	660
CAATCCATTC	ACTTGGGAGG	AGTATTTGAA	TTGCAACCAG	GTGCTTCGGT	GTTTGTCAAT	720
GTGACTGATC	CAAGCCAAGT	GAGCCATGGC	ACTGGCTTCA	CGTCCTTTGG	CTTACTCAAA	780
CTCTGA						786

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGATCGAAA	CATACAACCA	AACTTCTCCC	CGATCTGCGG	CCACTGGACT	GCCCATCAGC	60
ATGAAAATTT	TTATGTATTT	ACTTACTGTT	TTCCTTATCA	CCCAAATGAT	TGGATCTGTG	120
CTTTTTGCTG	TGTATCTTCA	TAGAAGATTG	GATAAGGTCG	AAGAGGAAGT	AAACCTTCAT	180
GAAGATTTTG	TATTCATAAA	AAAGCTAAAG	AGATGCAACA	AAGGAGAAGG	ATCTTTATCC	240
TTGCTGAACT	GTGAGGAGAT	GAGAAGGCAA	TTTGAAGACC	TTGTCAAGGA	TATAACGTTA	300
AACAAAGAAG	AGAAAAAAGA	AAACAGCTTT	GAAATGCAAA	GAGGTGATGA	GGATCCTCAA	360
ATTGCAGCAC	ACGTTGTAAG	CGAAGCCAAC	AGTAATGCAG	CATCCGTTCT	ACAGTGGGCC	420
AAGAAAGGAT	ATTATACCAT	GAAAAGCAAC	TTGGTAATGC	TTGAAAATGG	GAAACAGCTG	480
ACGGTTAAAA	GAGAAGGACT	CTATTATGTC	TACACTCAAG	TCACCTTCTG	CTCTAATCGG	540
GAGCCTTCGA	GTCAACGCCC	ATTCATCGTC	GGCCTCTGGC	TGAAGCCCAG	CATTGGATCT	600
GAGAGAATCT	TACTCAAGGC	GGCAAATACC	CACAGTTCCT	CCCAGCTTTG	CGAGCAGCAG	660
TCTGTTCACT	TGGGCGGAGT	GTTTGAATTA	CAAGCTGGTG	CTTCTGTGTT	TGTCAACGTG	720
ACTGAAGCAA	GCCAAGTGAT	CCACAGAGTT	GGCTTCTCAT	CTTTTGGCTT	ACTCAAACTC	780
TGA						783

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 786 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

ATGATAGAAA	CATACAGCCA	ACCTTCCCCC	AGATCCGTGG	CAACTGGACT	TCCAGCGAGC	60
ATGAAGATTT	TTATGTATTT	ACTTACTGTT	TTTCTTATCA	CCCAGATGAT	TGGGTCAGCA	120
CTTTTTGCTG	TGTATCTTCA	TAGAAGGTTG	GACAAGATAG	AAGATGAAAG	GAATCTTCAT	180
GAAGATTTTG	TATTCATGAA	AACGATACAG	AGATGCAACA	CAGGAGAAAG	ATCCTTATCC	240
TTACTGAACT	GTGAGGAGAT	TAAAAGCCAG	TTTGAAGGCT	TTGTGAAGGA	TATAATGTTA	300

CAAATTGCGG GCTGAAAAAG CTGACCGTTA CGGGAAGCTT TTCGAGAGAA CAATCCATTC GTGACTGATC	AGACGAAGAA CACATGTCAT GATACTACAC AAAGACAAGG CGAGTCAAGC TCTTACTCAG ACTTGGGAGG CAAGCCAAGT	AAGTGAGGCC CATGAGCAAC ACTCTATTAT TCCATTTATA AGCTGCAAAT AGTATTTGAA	AGCAGTAAAA AACTTGGTAA ATCTATGCCC GCCAGCCTCT ACCCACAGTT TTGCAACCAG	CAACATCTGT CCCTGGAAAA AAGTCACCTT GCCTAAAGTC CCGCCAAACC GTGCTTCGGT	GTTACAGTGG TGGGAAACAG CTGTTCCAAT CCCCGGTAGA TTGCGGGCAA GTTTGTCAAT	360 420 480 540 600 660 720 780
CTCTGA	CARGCCARGI	GAGCCATGGC	ACIGGCIICA	CGICCIIIGG	CITACICAAA	786

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 786 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATGATAGAAA	CATACAGCCA	ACCTTCCCCC	AGATCCGTGG	CAACTGGACT	TCCAGCGAGC	60
ATGAAGATTT	TTATGTATTT	ACTTACTGTT	TTCCTTATCA	CCCAAATGAT	TGGATCTGTG	120
CTTTTTGCTG	TGTATCTTCA	TAGAAGGTTG	GACAAGATAG	AAGATGAAAG	GAATCTTCAT	180
GAAGATTTTG	TATTCATGAA	AACGATACAG	AGATGCAACA	CAGGAGAAAG	ATCCTTATCC	240
TTACTGAACT	GTGAGGAGAT	TAAAAGCCAG	TTTGAAGGCT	TTGTGAAGGA	TATAATGTTA	300
AACAAAGAGG	AGACGAAGAA	AGAAAACAGC	TTTGAAATGC	AAAAAGGTGA	TCAGAATCCT	360
CAAATTGCGG	CACATGTCAT	AAGTGAGGCC	AGCAGTAAAA	CAACATCTGT	GTTACAGTGG	420
GCTGAAAAAG	GATACTACAC	CATGAGCAAC	AACTTGGTAA	CCCTGGAAAA	TGGGAAACAG	480
CTGACCGTTA	AAAGACAAGG	ACTCTATTAT	ATCTATGCCC	AAGTCACCTT	CTGTTCCAAT	540
CGGGAAGCTT	CGAGTCAAGC	TCCATTTATA	GCCAGCCTCT	GCCTAAAGTC	CCCCGGTAGA	600
TTCGAGAGAA	TCTTACTCAG	AGCTGCAAAT	ACCCACAGTT	CCGCCAAACC	TTGCGGGCAA	660
CAATCCATTC	ACTTGGGAGG	AGTATTTGAA	TTGCAACCAG	GTGCTTCGGT	GTTTGTCAAT	720
GTGACTGATC	CAAGCCAAGT	GAGCCATGGC	ACTGGCTTCA	CGTCCTTTGG	CTTACTCAAA	780
CTCTGA						786

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 864 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

AACTCTAACG	CAGCATGATC	GAAACATACA	GTCAACCTTC	TCCCCGCTCC	GTGGCCACTG	60
GACCACCTGT	CAGTATGAAA	ATTTTTATGT	ATTTACTTAC	AGTTTTTCTT	ATCACCCAGA	120
TGATTGGGTC	AGCGCTTTTT	GCTGTGTATC	TTCACAGACG	ATTGGACAAG	ATAGAAGACG	180

3 3 3 CC 3 3 CC	maxmaxxaxm	mmmamamma	ma			
			TGAAAACGAT			240
AGGGGTCCTT	ATCCTTACTG	AACTGTGAGG	AAATTAGAAG	CCGGTTTGAA	GACTTGGTCA	300
AGGATATAAT	GCAAAACAAA	GAAGTAAAGA	AGAAAGAAAA	AAACTTTGAA	ATGCACAAGG	360
GTGATCAGGA	GCCTCAGATA	GCGGCACATG	TCATCAGTGA	GGCCAGTAGT	AAAACAACCT	420
CTGTTCTCCA	GTGGGCCCCC	AAAGGATACT	ACACCCTAAG	CAACAACCTG	GTAACCCTCG	480
AAAACGGGAA	ACAGCTGGCC	GTGAAAAGAC	AAGGATTCTA	TTACATCTAC	ACCCAAGTCA	540
CCTTCTGTTC	CAATCGGGAA	ACTTTGAGTC	AAGCTCCATT	TATAGCCAGC	CTCTGCCTGA	600
AGTCCCCAAG	TGGATCAGAG	AGAATCTTAC	TGAGAGCTGC	AAACACCCAC	AGTTCTTCCA	660
AACCATGCGG	GCAGCAATCC	ATTCACTTAG	GAGGAGTCTT	TGAATTGCAA	TCGGGTGCTT	720
CGGTGTTTGT	CAATGTGACT	GATCCAAGTC	AAGTGAGCCA	CGGGACGGGC	TTCACATCAT	780
TTGGCTTACT	CAAACTCTGA	ACGGTGTAAG	CCAGCAGGCT	GCGGCTGGGC	TGATGCTGGT	840
GGTCTTCACA	ATCCAGGAAA	GCAG				864

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3634 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GAATTCCGGG	TGATTTCACT	CCCGGCTGTC	CAGGCTTGTC	CTGCTACCCC	ACCCAGCCTT	60
TCCTGAGGCC	TCAAGCCTGC	CACCAAGCCC	CCAGCTCCTT	CTCCCCGCAG	GACCCAAACA	120
CAGGCCTCAG	GACTCAACAC	AGCTTTTCCC	TCCAACCCGT	TTTCTCTCCC	TCAACGGACT	180
	AAGCCCCTCC		TCTATCTTTT	TCCTGCATCC	TGTCTGGAAG	240
TTAGAAGGAA	ACAGACCACA	GACCTGGTCC	CCAAAAGAAA	TGGAGGCAAT	AGGTTTTGAG	300
GGGCATGGGG	ACGGGGTTCA	GCCTCCAGGG	TCCTACACAC	AAATCAGTCA	GTGGCCCAGA	360
AGACCCCCCT	CGGAATCGGA	GCAGGGAGGA	TGGGGAGTGT	GAGGGGTATC	CTTGATGCTT	420
GTGTGTCCCC	AACTTTCCAA	ATCCCCGCCC	CCGCGATGGA	GAAGAAACCG	AGACAGAAGG	480
TGCAGGGCCC	ACTACCGCTT	CCTCCAGATG	AGCTCATGGG	TTTCTCCACC	AAGGAAGTTT	540
TCCGCTGGTT	GAATGATTCT	TTCCCCGCCC	TCCTCTCGCC	CCAGGGACAT	ATAAAGGCAG	600
TTGTTGGCAC	ACCCAGCCAG	CAGACGCTCC	CTCAGCAAGG	ACAGCAGAGG	ACCAGCTAAG	660
AGGGAGAGAA	GCAACTACAG	ACCCCCCTG	AAAACAACCC	TCAGACGCCA	CATCCCCTGA	720
CAAGCTGCCA	GGCAGGTTCT	CTTCCTCTCA	CATACTGACC	CACGGCTTCA	CCCTCTCTCC	780
	ACACCATGAG		ATGATCCGGG	ACGTGGAGCT	GGCCGAGGAG	840
GCGCTCCCCA	AGAAGACAGG	GGGGCCCCAG	GGCTCCAGGC	GGTGCTTGTT	CCTCAGCCTC	900
TTCTCCTTCC	TGATCGTGGC	AGGCGCCACC	ACGCTCTTCT	GCCTGCTGCA	CTTTGGAGTG	960
ATCGGCCCCC	AGAGGGAAGA	GGTGAGTGCC	TGGCCAGCCT	TCATCCACTC	TCCCACCCAA	1020
GGGGAAATGA	GAGACGCAAG	AGAGGGAGAG	AGATGGGATG	GGTGAAAGAT	GTGCGCTGAT	1080
AGGGAGGGAT	GAGAGAGAAA	AAAACATGGA	GAAAGACGGG	GATGCAGAAA	GAGATGTGGC	1140
AAGAGATGGG	GAAGAGAGAG	AGAGAAAGAT	GGAGAGACAG	GATGTCTGGC	ACATGGAAGG	1200
TGCTCACTAA	GTGTGTATGG	AGTGAATGAA	TGAATGAATG	AATGAACAAG	CAGATATATA	1260
AATAAGATAT	GGAGACAGAT	GTGGGGTGTG	AGAAGAGAGA	TGGGGGAAGA	AACAAGTGAT	1320
ATGAATAAAG	ATGGTGAGAC	AGAAAGAGCG	GGAAATATGA	CAGCTAAGGA	GAGAGATGGG	1380
GGAGATAAGG	AGAGAAGAAG	ATAGGGTGTC	TGGCACACAG	AAGACACTCA	GGGAAAGAGC	1440
TGTTGAATGC	TGGAAGGTGA	ATACACAGAT	GAATGGAGAG	AGAAAACCAG	ACACCTCAGG	1500
GCTAAGAGCG	CAGGCCAGAC	AGGCAGCCAG	CTGTTCCTCC	TTTAAGGGTG	ACTCCCTCGA	1560
TGTTAACCAT	TCTCCTTCTC	CCCAACAGTT	CCCCAGGGAC	CTCTCTCTAA	TCAGCCCTCT	1620
GGCCCAGGCA	GTCAGTAAGT	GTCTCCAAAC	CTCTTTCCTA	ATTCTGGGTT	TGGGTTTGGG	1680
GGTAGGGTTA	GTACCGGTAT	GGAAGCAGTG	GGGGAAATTT	AAAGTTTTGG	TCTTGGGGGA	1740
GGATGGATGG	AGGTGAAAGT	AGGGGGGTAT	TTTCTAGGAA	GTTTAAGGGT	CTCAGCTTTT	1800
TCTTTTCTCT	CTCCTCTTCA	GGATCATCTT	CTCGAACCCC	GAGTGACAAG	CCTGTAGCCC	1860
ATGTTGTAGG	TAAGAGCTCT	GAGGATGTGT	CTTGGAACTT	GGAGGGCTAG	GATTTGGGGA	1920
TTGAAGCCCG			GGAGACAATG	TGAGAAGGAC	TCGCTGAGCT	1980
CAAGGGAAGG	GTGGAGGAAC	AGCACAGGCC	TTAGTGGGAT	ACTCAGAACG	TCATGGCCAG	2040

GTGGGATGTG GGATGACAGA CAGAGAGGAC AGGAACCGGA TGTGGGGTGG GCAGAGCTCG AGGGCCAGGA TGTGGAGAGT GAACCGACAT GGCCACACTG ACTCTCCTCT CCCTCTCTCC CTCCCTCCAG CAAACCCTCA AGCTGAGGGG CAGCTCCAGT GGCTGAACCG CCGGGCCAAT 2220 GCCCTCCTGG CCAATGGCGT GGAGCTGAGA GATAACCAGC TGGTGGTGCC ATCAGAGGGC 2280 CTGTACCTCA TCTACTCCCA GGTCCTCTTC AAGGGCCAAG GCTGCCCCTC CACCCATGTG 2340 CTCCTCACCC ACACCATCAG CCGCATCGCC GTCTCCTACC AGACCAAGGT CAACCTCCTC 2400 TCTGCCATCA AGAGCCCTG CCAGAGGGAG ACCCCAGAGG GGGCTGAGGC CAAGCCCTGG TATGAGCCCA TCTATCTGGG AGGGGTCTTC CAGCTGGAGA AGGGTGACCG ACTCAGCGCT 2520 GAGATCAATC GGCCCGACTA TCTCGACTTT GCCGAGTCTG GGCAGGTCTA CTTTGGGATC 2580 ATTGCCCTGT GAGGAGGACG AACATCCAAC CTTCCCAAAC GCCTCCCCTG CCCCAATCCC 2640 TTTATTACCC CCTCCTTCAG ACACCCTCAA CCTCTTCTGG CTCAAAAAGA GAATTGGGGG CTTAGGGTCG GAACCCAAGC TTAGAACTTT AAGCAACAAG ACCACCACTT CGAAACCTGG GATTCAGGAA TGTGTGGCCT GCACAGTGAA GTGCTGGCAA CCACTAAGAA TTCAAACTGG 2820 GGCCTCCAGA ACTCACTGGG GCCTACAGCT TTGATCCCTG ACATCTGGAA TCTGGAGACC 2880 AGGGAGCCTT TGGTTCTGGC CAGAATGCTG CAGGACTTGA GAAGACCTCA CCTAGAAATT 2940 GACACAAGTG GACCTTAGGC CTTCCTCTCT CCAGATGTTT CCAGACTTCC TTGAGACACG 3000 GAGCCCAGCC CTCCCCATGG AGCCAGCTCC CTCTATTTAT GTTTGCACTT GTGATTATTT 3060 ATTATTTATT TATTATTTAT TTATTTACAG ATGAATGTAT TTATTTGGGA GACCGGGGTA 3120 TCCTGGGGGA CCCAATGTAG GAGCTGCCTT GGCTCAGACA TGTTTTCCGT GAAAACGGAG CTGAACAATA GGCTGTTCCC ATGTAGCCCC CTGGCCTCTG TGCCTTCTTT TGATTATGTT TTTTAAAATA TTTATCTGAT TAAGTTGTCT AAACAATGCT GATTTGGTGA CCAACTGTCA CTCATTGCTG AGCCTCTGCT CCCCAGGGGA GTTGTGTCTG TAATCGCCCT ACTATTCAGT GGCGAGAAAT AAAGTTTGCT TAGAAAAGAA ACATGGTCTC CTTCTTGGAA TTAATTCTGC 3420 ATCTGCCTCT TCTTGTGGGT GGGAAGAAGC TCCCTAAGTC CTCTCCAC AGGCTTTAAG ATCCCTCGGA CCCAGTCCCA TCCTTAGACT CCTAGGGCCC TGGAGACCCT ACATAAACAA AGCCCAACAG AATATTCCCC ATCCCCCAGG AAACAAGAGC CTGAACCTAA TTACCTCTCC 3600 CTCAGGGCAT GGGAATTTCC AACTCTGGGA ATTC 3634

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1997 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GAGACAGAGT CTTGCTCTGT CCCCCAGGCT GGAATACAGT GGTGCGATCT TGACTCACTG 60 CAGCCTCCGC CTCCCAGGTT CAAATAATTC TCCAGCCTCA GCCTCCCGAG TAGCTGGGAC 120 TGCAGATGCG CACCAGCACG CCTGGCTAAT TTTTGTATTT ATTATAGAGA TGGGGTTTCA CCATGTTGGC CAGCTGGTCT CAAACTCCTG ACCTCAAGTA ATCCGCCCAC CTCAGACTCC CAAAGTGCCA GGATTACAGG TGTGAGCCAC TGCACCAGGC CTGGAACAAT TTTAAAATAA TGTATTGGCT CTGCAAATGC AGCTTCAGAA CAAGTCCCTT AGCTGTCCCC ACCCCACCCT AAGTCACCAC CCTTAAGCCT CACCCATGTG GAATTCTGAA ACTTCCTTTG TAGAAAACTT TGGAAGGTGT CTGCCACATT GATCCTGGAA TGTGTGTTTA TTTGGGGTTA TATAAATCTG 480 TTCTGTGGAA GCCACCTGAA GTCAGGAAGA GATGGAGGGC ATCCTTCAGG AGTGAGATGA 540 GACCTCATCA TACTTGACTG TCCAGCATCA TCTCTGAGTA AGGGGACCAA AAAATTTATC 600 TTCCAAACTA GGACACTTTC AAGAGTGGAA GGGGGATCCA TTAATATTTT CACCTGGACA 660 AGAGGCAAAC ACCAGAATGT CCCCGATGAA GGGGATATAT AATGGACCTT CTTGATGTGA 720 AACCTGCCAG ATGGGCTGGA AAGTCCGTAT ACTGGGACAA GTATGATTTG AGTTGTTTGG GACAAGGACA GGGGTACAAG AGAAGGAAAT GGGCAAAGAG AGAAGCCTGT ACTCAGCCAA GGGTGCAGAG ATGTTATATA TGATTGCTCT TCAGGGAACC GGGCCTCCAG CTCACACCCC 900 AGCTGCTCAA CCACCTCCTC TCTGAATTGA CTGTCCCTTC TTTGGAACTC TAGGCCTGAC 960 CCCACTCCCT GGCCCTCCCA GCCCACGATT CCCCTGACCC GACTCCCTTT CCCAGAACTC 1020 AGTCGCCTGA ACCCCCAGCC TGTGGTTCTC TCCTAGGCCT CAGCCTTTCC TGCCTTTGAC

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TGAAACAGCA	GTATCTTCTA	AGCCCTGGGG	GCTTCCCCGG	GCCCCAGCCC	CGACCTAGAA	1140
CCCGCCCGCT	GCCTGCCACG	CTGCCACTGC	CGCTTCCTCT	ATAAAGGGAC	CTGAGCGTCC	1200
GGGCCCAGGG	GCTCCGCACA	GCAGGTGAGG	CTCTCCTGCC	CCATCTCCTT	GGGCTGCCCG	1260
TGCTTCGTGC	TTTGGACTAC	CGCCCAGCAG	TGTCCTGCCC	TCTGCCTGGG	CCTCGGTCCC	1320
TCCTGCACCT	GCTGCCTGGA	TCCCCGGCCT	GCCTGGGCCT	GGGCTTGGTG	GGTTTGGTTT	1380
TGGTTTCCTT	CTCTGTCTCT	GACTCTCCAT	CTGTCAGTCT	CATTGTCTCT	GTCACACATT	1440
CTCTGTTTCT	GCCATGATTC	CTCTCTGTTC	CCTTCCTGTC	TCTCTCTGTC	TCCCTCTGCT	1500
CACCTTGGGG	TTTCTCTGAC	TGCATCTTGT	CCCCTTCTCT	GTCGATCTCT	CTCTCGGGGG	1560
TCGGGGGGTG	CTCTCTCCCA	GGGCGGGAGG	TCTGTCTTCC	GCCGCGTGCC	CCGCCCCGCT	1620
CACTGTCTCT	CTCTCTCTCT	CTCTTTCTCT	GCAGGTTCTC	CCCATGACAC	CACCTGAACG	1680
TCTCTTCCTC	CCAAGGGTGT	GTGGCACCAC	CCTACACCTC	CTCCTTCTGG	GGCTGCTGCT	1740
GGTTCTGCTG	CCTGGGGCCC	AGGTGAGGCA	GCAGGAGAAT	GGGGGCTGCT	GGGGTGGCTC	1800
AGCCAAACCT	TGAGCCCTAG	AGCCCCCTC	AACTCTGTTC	TCCCCTAGGG	GCTCCCTGGT	1860
GTTGGCCTCA	CACCTTCAGC	TGCCCAGACT	GCCCGTCAGC	ACCCCAAGAT	GCATCTTGCC	1920
CACAGCACCC	TCAAACCTGC	TGCTCACCTC	ATTGGTAAAC	ATCCACCTGA	CCTCCCAGAC	1980
ATGTCCCCAC	CAGCTCT					1997

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10240 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GAATTCCCCG	GATCAAAGTC	AGCATTAAAT	CCCAGTTTAG	GTTTTGAGGC	TAAGTTCAAG	60
TTTGAGTCTA	ATGTCATTTC	AGCCTTGTTT	GGAGGACTCA	GAGATTTCAC	TAGTTTCTCC	120
GCAGAGACCA	CTGTAGAAAC	TGCATTTCCC	TGAGTTTTGG	GCACAAGACT	CCAGTCATCA	180
CCCCTCCCAC	ACAGGGAAAG	CCCCAAACCA	ACTGCTGGCC	TCCTCAAGAA	AGAAACCGAA	240
TTTCACACAA	CCTCCGAAAC	TAAGATTGAA	ACCAAGATTG	GCCCATCTCA	AGGCGCGTCC	300
TCCAGCACAT	TGAGAATGTC	GCTGATGGAG	CCTCGGCCCA	GCTCTCGAGC	TTCCTTCCTT	360
TCTGTCTCTC	ATGTCTTCTC	ATCACTCCTT	CTCACCTTCC	CGTTTTTGTC	CTGCAATGCC	420
CCCTTCTTCC	TCTCTTCCTG	GGGTTTTTCC	CTTTATTTCT	CACTGTACCA	TTTTATATTT	480
TAATAAAGCC	GAGGTCTCCT	AGTCCATCAG	CTCCTACTGT	TGGAGAGGAG	GCAGAAAGAA	540
ACAGCAGGAC	GGCAAAGGGA	CTCCAGAGAA	AGAGACTCAG	AGGAAAGGCA	AGAAACAGGG	600
ACCAAGAGAG	AGGCCAACAG	TGACACAAGA	CACAGTGAGG	TTAAAAGAAA	TAAGATGAGG	660
CCAAGATAGA	GACCAAGCTA	TTTAAAAGAG	CCATCTGTGG	CTACCCTTCT	TCCGCCATCG	720
CATCTGGTCA	GCCACCAAGA	TTTTGCCTAG	AAACGTTCCT	CCTCTCCATT	CTCCTGCTGC	780
TGCTGCTGCT	GCTGCTGCTG	CTGCTGCTGC	TGCTGCTGCT	GCTGCTGCTG	CTGCCTTAAT	840
ACGAATGCAG	GCTCTTGTCA	TCTCCTTGCT	GGGTTGTTGC	AAAATCCTCC	TAACTGGTCT	900
CCACACTTCT	CATTTCCCCT	CCAGCCCCCC	ATCTTCCATA	CTTCCATTTA	TTTATTTTGG	960
CCATGCCCAT	GGCATGTGGC	AGTTCCAGGG	GCCAGGGATC	AAACCTGTGC	CAATGCAGTG	1020
ACCGTGTCAG	ATCCTTAACC	CACTGCACAC	AAGGCAACGC	CCCTCGAGTC	ATTCTCATTT	1080
TTTAAATATA	CCAATTTGAG	GGGGTCCCTC	TTTCACTTAA	AAATTTTGGC	AGCTCCCTAT	1140
CATGATGAGA	AGGAATTCCA	AACCATTTTT	CTTGTGTGCA	AACCCTTCAG	CATGTGTCCT	1200
CAGCTTACTT	CCCAAGCCTC	ATCCCTGCTC	CTTCTACGTG	TACCCATGTG	TACATCTCCA	1260
CACACCATAT	ACTCTTTTTT	ACCTCCCATC	TTTGCACCTT	CTGTTCCCTC	TCTCTGCCCC	1320
TCACCATCTT	TTTTGCTTTG	ATACTTAATG	CCTCTCCCTC	AGGCCAGGTT	CAATGGCTTT	1380
TCTGTGGGCT	GCTTTAAGCC	CACTGTCATG	GAACTTATCA	CATTTTATTT	TATTTGACTT	1440
TCTTTTTAGG	GCCGCACCCA	GCATATGGAG	ATTCCCAGGC	TAGGGATCTA	ATCGGAGCTG	1500
TATCTGCCAG	CCTGCGCTGG	AGCCACAGCA	ACGTGGGATC	CGAGCCTGAG	GGGTTTTGAT	1560
GTCCTGTGGC	ACAGAAGTTA	CATTCAGGCT	GTGCATGAAC	TATTTCTCCT	GTTCTCCTCC	1620
CCCTGCTTGA	GGCCCTGCAG	CTTTGCCTCT	CATGCCTTGC	TGCTCTGACC	TATGACTTCT	1680
TTTTGTTTGC	ATTCCATCTC	TTTAGTTTTC	TCTCTGTTCC	ACAAACATTT	ACTGAGCATC	1740
TACATGAGGC	ATTGAGGATA	CGGATGGGAA	AGACAGTCCC	CTGACCTCTG	GGACCTCAAA	1800
GACCAATTGT	GGAAGACTGG	TTGGTTATCA	GATAATTACA	ATGAAGTGTG	GGAGTCCCTG	1860

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

Kipps, Thomas J. Sharma, Sanjai Cantwell, Mark

(ii) TITLE OF INVENTION:

NOVEL EXPRESSION VECTORS
CONTAINING ACCESSORY
MOLECULE LIGAND GENES AND
THEIR USE FOR IMMUNO-

MODULATION AND TREATMENT OF

MALIGNANCIES

(iii) NUMBER OF SEQUENCES:

44

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:

Lyon & Lyon

(B) STREET:

633 West Fifth Street

Suite 4700

(C) CITY:

(D)

Los Angeles California

(E) COUNTRY:

U.S.A.

(F) ZIP:

90071-2066

(v) COMPUTER READABLE FORM:

STATE:

(A) MEDIUM TYPE:

3.5" Diskette, 1.44 Mb storage

(B) COMPUTER:

IBM Compatible

(C) OPERATING SYSTEM:

IBM P.C. DOS 5.0

(D) SOFTWARE:

FastSeq Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

To Be Assigned

(B) FILING DATE:

(C) CLASSIFICATION:

				AGGATGCAGA		1920
				CTGTGGTGTA		1980
				GGTGGCTACC		2040
				AAAAAAAAGA		2100
				GGCTCCTATT		2160
				GTTCCCGTCG		2220
GAAACAAATT	CGACTAGGAA	CCATGAGGTT	GCGGGTTCGA	TCCCTGGCCT	TGCTCAGTGG	2280
GTTAAGGATC	CGGCGTTGCC	GTGAGCTGTG	GTGTAGGTCG	CAGATGTGGC	TCGGATCTAG	2340
TGTTGCTGTG	GCTCTGGTGT	AGGCCGGCAG	CAACAGCTCT	GATTAGACTC	CTAGCCTGAG	2400
AACCTCCATA	AGCTGTGGCT	GCGGCCCTAT	AAAGACAAAA	ААААААААА	GGCCAAATAC	2460
TAGAAACAAA	CCAAATGCCC	ATCAACAGAA	GAATAGATAA	GTTAATTGGG	GTATATGCAC	2520
ACAATAGCAT	CACACAATAA	CATGCACACA	ATAACATCAC	AATGAAATAA	AAATTACTAC	2580
TGACAGACAC	AACCATATAG	ATGAATTTCA	CAAACACAAC	AGCGAGAATA	AAAGCCAAGC	2640
				AAGCGCAGGA		2700
CTATAGTGAC	AGAGGTCAGA	GAGCAGTTGG	TTGTCTTTGG	CAGGTATGAA	CTGGGAGTGG	2760
				TGGATGGTGG		2820
ACAAGAAGAT	GGAAAAGTTC	CTCAGGCTGT	CCACTTGGGA	GACGGGCTTC	TCACGGGACC	2880
TAAGTTCTGC	ATCAGCAGAG	GGGGAAATCC	TTAATGATTT	GACAATTACA	AAGTGTATTG	2940
				CCACCCCACC		3000
				TGTAGAGAAC		3060
				GACACATCTG		3120
				AGTGAGATGA		3180
				AATGAGGACA		3240
				AACAAACCAG		3300
				CCAGATGACC		3360
				GACAGGGGTA		3420
				GAGGTGTTAT		3480
				CTCCATCTCC		3540
				CCCTGGCCCT		3600
				CTGAGCCCCC		3660
				GCAGCATCTT		3720
GGCTTCCCCA	GGCCCCAGCC	CCGGCCTAGA	ACCCGCCCAG	CCGACCTGCC	CACGCTGCCA	3780
				AGGGGCCCAC		3840
				TCCGGGTGCT		3900
				CCTCCTGCAT		3960
				GATTCTTTAT		4020
				TCCCATCTCT		4080
				CTGGTCCCCT		4140
				GCAGGAGGCC		4200
				TTTCCCCATG		4260
GACGCCTCTA	CCTCCGGAGG	GTGTGCAGCA	CCCCCATCCT	CCTCCTCCTG	GGGCTGCTGC	4320
TGGCCCTGCC	GCCCGAGGCC	CAGGTGAGGC	AGCAGGAGAG	CGGGCCGTGG	GGGCAGCCTT	4380
					TCCCTGGCGT	
CGGCCTCCCA	CCCTCAGCTG	CACAGCCTGC	CCATCAGCAC	CCCCCAAAGC	ACTTGGCCAG	4500
AGGCACCCTC	AAACCTGCCG	CTCACCTCGT	TGGTAAACAT	CCACCTGGCC	TCCCAGACCT	4560
				TGAAGCATCC		4620
TCTCCCCCCA	CCCCCTAAAT	GGAGGCATCC	CACTCCCGAC	TCCCTCCCAA	CCATCCCCCA	4680
GGAACTCAGT	CCAGCACCTG	CTTCCTCAGG	GATTGAGACC	TCCGACCCCC	AGGTCCTTGA	4740
				CCGGACTCAC		4800
AGCGAACACG	GATCGTGCCT	TCCTCCGCCA	TGGCTTCTTG	CTGAGCAACA	ACTCCCTGCT	4860
GGTCCCCACC	AGTGGCCTCT	ACTTTGTCTA	CTCCCAGGTC	GTCTTCTCCG	GGGAAGGCTG	4920
CTTCCCCAAG	GCCACCCCCA	CCCCTCTCTA	CCTGGCCCAC	GAGGTCCAGC	TCTTCTCCTC	4980
				TCCGTGTGCC		5040
				CTGCTCACCC		5100
				AGCCCCAGTA		5160
				TTGGTTTCAA		5220
				CCTCTCCTCT		5280
				TGTAGAAGGA		5340
					CCGCCTGGAG	5400
				ACGTGGAAGG		5460
						3400

CATGAGGGAC	TTTGAACGGA	TGACCGGAGC	GGTGTGGGGG	GGTTATTTAT	GAAGGGGAAA	5520
ATTAAATTAT	TTATTTATGG	AGGATGGAGA	GAAGGGAATC	ACAGAGGGAT	GTCAGAAGAG	5580
TGTGACACAT	GTGCCCAAGA	GATAAAGTGA	CAGAAGGCAT	GGGCTCCAGA	TGACCCGGCC	5640
AGAGAGGCA	AAGTGGCTCA	GGAAGGGGCT	GCTTGACTGG	AGGCTCATGA	GGAGACGGCT	5700
GACCCTCGAT	GAAACCCAAT	AAAGCTCTTT	TCTCTGAAAT	GCTGTCTGCT	CGTATCTGTC	5760
ACTCGGGAGG	GGAGAATTCT	CCAGATGTCT	CTAAGGAGTG	GAGGGAGGAC	AGGAATCAGA	5820
GGGGACGGGA	GCTGTGGGTG	TGTGATGAGG	CCTAAGGGGC	TCAGGTGAGA	GATGGCGGCC	5880
TCAGGGTGAG	GGCAGCCAGA	CCCCTGCAGG	AGAAGCAGAT	GGTTCCTCTG	AGAAGACAAA	5940
GGAAGAGATG	CAGGGCCAAG	GTCTTGAGAA	CCGAGGTCGG	GGGTCGCCTG	GCAGATATGG	6000
CCACAGGTAG	AGGGACAGAG	GAATAGGGGT	GACAGGAGGC	TTCCCGGGAG	AAGGGAACAC	6060
ACTGAGGGGT	GTTCGGGATT	CTGAGGGAGG	AGCACGGGGA	CGCCCTGGGA	GACATGCCGT	6120
CCAGGGCCAT	GAGGAGTGGG	AGAGCCTCTG	AGGCTAGCGG	CTGGAGATAC	AGGGACATTT	6180
GAGGAGACAC	GGTCATGGCC	AGGAGCCGCG	AGGGCCTGGA	CAGTCTCTAG	GAATCTCGAA	6240
GAAGCAGGAA	TTCTTTGAGG	ATACGTGGCC	ACACAAAGGG	AGGCTGAGGT	GTGGGGACTT	6300
CATGCAGAAG	TCAGGGCCTC	ACATTCCCTT	GGAAGCCGAG	ACTGAAACCA	GCAGCAGAGT	6360
TTTGGTGAGT	TCCTGTCAGA	GTGAAAGGAG	AAGGCCCGCC	ATGGTGGGTT	TGTGAATTCC	6420
CAGCCTGGCT	TCCTCTCCCT	CTGGGGCTGT	CCCAGGCCTG	TTCCTGCCGT	CCTCCCCCAG	6480
CCCGTGTAGG	GCCTCCAGCT	GCCCTTCTCC	CAGCTCCTCT	TCCCTCCAGG	AGACGAAACA	6540
TGGGTCTCAG	CACCCAGCGC	GGTGTCGTCT	AAGTTTTCTC	TCCATTAAGA	ACTCAGCTTT	6600
CTGAAGCTCC	TCCCATTCCT	AGTTCTACCC	CTACCTGAGC	CCTGTTCGGA	AATCAGAGAG	6660
AAATAGAAGT	CATCCCCCAA	AGAAAAGGAA	TTTGTCCCCC	AAAGAAACAG	AACTTGTCCC	6720
CCAAAGAAAT	GGAAACAATG	GGAAATGGGA	GGCAGGGGGG	ACCTGGGGTC	CAGCCTCCAG	6780
GGTCCTACAC	ACAGAGCAGT	AACTGGCCCA	GCAAGCCCAC	CTCAGGATCC	GGGCAGGGAG	6840
GGTAGGAAGT	ATCCCTGATG	CCTGGGTGTC	CCCAACTTTC	CAAACCGCCG	CCCCCGCTAT	6900
GGAGATGAAA	CTAAGACAGA	AGGTGCAGGG	CCCGCTACCG	CTTCCTCCAG	ATGAGCTCAT	6960
GGGTTTCTCC	ACCAAGGAAG	TTTTCCGCTG	GTTGAAAGAG	AGCCTCTCCC	CGCCCTCTTC	7020
TCACCCAGAG	CGTATAAATG	CAGCTGTTTG	CACACCCAGC	CAGCAGAAGC	TCCCAGAGTG	7080
AGGACACCAG	GGGACCAGCC	AGGAGAGA	CAAGCCATCT	CCAGGACCCC	CTAGAAATAA	7140
CCTCTCAGAA	GACACACCCC	CGAACAGGCA	GCCGGACGAC	TCTCTCCCTC	TCACACGCTG	7200
CCCCGGGGCG	CCACCATCTC	CCAGCTGGAC	CTGAGCCCCT	CTGAAAAAGA	CACCATGAGC	7260
ACTGAGAGCA	TGATCCGAGA	CGTGGAGCTG	GCGGAGGAGG	CGCTCGCCAA	GAAGGCCGGG	7320
GGCCCCCAGG	GCTCCAGGAG	GTGCCTGTGC	CTCAGCCTCT	TCTCCTTCCT	CCTGGTCGCA	7380
		CCTACTGCAC				7440
GTGAGCGCCT	GGCCAGCCTT	GGCTCATTCT	CCCACCCGGA	GAGAAATGGG	GAAGAAAGAG	7500
		AAAGAAGTGT				7560
		AGGAGACGTG				7620
GAGAGAAATC	CGGTGGCCCG	GCCCTTGGAA	ATGCTCTCTA	AATATTTGTT	GCACGAATGA	7680
		ATATAAAGAG				7740
		TGATCTGGAT				7800
		AGAGAAGAAG				7860
		ATGGATGGGT				7920
		AGTACAAGCT				7980
		TTAATCCTTC				8040
		CCCAAGGACT				8100
		GGGGTTAGTG				8160
		ATGCAGGTCA				8220
		CTCTTTCCTC				8280
		GTAAGAGTTC				8340
		ATTTGGGGGC				8400
		CGCTGAGCTC				8460
		ATGGACAGAT				8520
		GCAGAACTCG				8580
		TCCCTCTTTG				8640
		GTGGGTATGC				8700
		TGCCGACAGA				8760
		CTTCCACCAA				8820
		AGGTCAACCT				8880
		AGGCCAAGCC				8940
		ATCGACTCAG				9000
CTTTGCTGAA	TCTGGGCAGG	TCTATTTTGG	GATCATTGCC	CTGTGAGGGG	GCAGGACATC	9060

CGTTCCCTCC CCTGTCCATC CCTTTATTAT TTTACTCCTT CAGACCCCCT CACGTCCTTC 9120 TGGTTTAGAA AGAGAATGAG GGGCTGGGGA CTGGGCTCCA AGCTTAAAAC TTTAAACAAC AACAGCAACA CTTAGAAATC AGGGATTCAG GGATGTGTGG CCTGGACAAC CAGGCACTGA 9240 CCACCACA GAATTGGAAC TGGGGCTTCC AGACTCGCTG GGGTCCTTGG GTTTGGATTC 9300 CTGGATGCAA CCTGGGACAT CTGGAATGTG GCTGCCAGGG AAGCTTGGGT TCCAATCGGA 9360 ATACTTCAGA ACATTCCTTG AGAAGATTTC ACCTCAATCT TGATGACTTT TTAGGCTTCC 9420 CTTTCTTCCA ATTTTCCAGA CTTCCCTGGG ATGGGGAGCC CAGCCCCAAA CCCCACAGGC 9480 CAGCTCCCTC TTATTTATAT TTGCACTTGG CATTATTATT TATTTATTTA TTTATTATTT 9540 ATTTACTAGT GAATGTATTT ATTCAGGAGG GCGAGGTGTC CTGGGAGACC CAGCATAAGG 9600 GCTGCCTTGG TTCAGATGTG TTTTCTGTGA AAACGGAGCT GAACTGTAGG TTGCTCCCAC CTGGCCTCCT AGCCTCTGTG CCTCCTTTTG CTTATGTTTT TAAAAACAAA TATTTATCTG 9720 ATCGAGTTGT CTAAATAATG CTGATTTGGT GACTAACTTG TCGCTACATC GCTGAACCTC 9780 TGCTCCCAG GGGAGTTGTG TCTGTAACCG CCCTACTGGT CAGTGGCGAG AAATAAAAGC 9840 GTGCTTAGAA AAGAAATCTG GCCTCTTTCT GCGACTGAAT TCTGCATCTC CTTGGGGGGG 9900 TGAGGCTGCT CCCCAAAATT CTTTCTCCAC CGGGCTTAGG ATTCCCTGGG CTTCACTCCT 9960 GAGCTTGGAC TGCCTGGCTC AGGAGCCTCT GCAAGAACA AAGCCCAGCC AAACAGGTCC 10020 CTCCCCTAAG AAAGGAACCT GAAGGTAATT ACCTCTCCCT CAGGGTGTGG GAATTTCCAA 10080 GTCTGGGAAT TCCTATCCAG CTGGGGAAGT CTGCAGTGCA GGTGAGACTT CCGGCTGAAA GAGCCAGGGA GCGGCCAGAT GCTCAGGTAC CTGAACCAGA GCCAAGGGAC TTCCAGACAG 10200 TGAGGCAACT GGGCTCCAAA TAACCTGATC CGGGGAATTC 10240

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1644 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCTCAGCGAG GACAGCAAGG GACTAGCCAG GAGGGAGAAC AGAAACTCCA GAACATCCTG GAAATAGCTC CCAGAAAAGC AAGCAGCCAA CCAGGCAGGT TCTGTCCCTT TCACTCACTG 120 GCCCAAGGCG CCACATCTCC CTCCAGAAAA GACACCATGA GCACAGAAAG CATGATCCGC 180 GACGTGGAAC TGGCAGAAGA GGCACTCCCC CAAAAGATGG GGGGCTTCCA GAACTCCAGG 240 CGGTGCCTAT GTCTCAGCCT CTTCTCATTC CTGCTTGTGG CAGGGGCCAC CACGCTCTTC 300 TGTCTACTGA ACTTCGGGGT GATCGGTCCC CAAAGGGATG AGAAGTTCCC AAATGGCCTC 360 CCTCTCATCA GTTCTATGGC CCAGACCCTC ACACTCAGAT CATCTTCTCA AAATTCGAGT 420 GACAAGCCTG TAGCCCACGT CGTAGCAAAC CACCAAGTGG AGGAGCAGCT GGAGTGGCTG 480 AGCCAGCGCG CCAACGCCCT CCTGGCCAAC GGCATGGATC TCAAAGACAA CCAACTAGTG 540 GTGCCAGCCG ATGGGTTGTA CCTTGTCTAC TCCCAGGTTC TCTTCAAGGG ACAAGGCTGC 600 CCCGACTACG TGCTCCTCAC CCACACCGTC AGCCGATTTG CTATCTCATA CCAGGAGAAA 660 GTCAACCTCC TCTCTGCCGT CAAGAGCCCC TGCCCCAAGG ACACCCCTGA GGGGGCTGAG CTCAAACCCT GGTATGAGCC CATATACCTG GGAGGAGTCT TCCAGCTGGA GAAGGGGGAC CAACTCAGCG CTGAGGTCAA TCTGCCCAAG TACTTAGACT TTGCGGAGTC CGGGCAGGTC 840 TACTTTGGAG TCATTGCTCT GTGAAGGGAA TGGGTGTTCA TCCATTCTCT ACCCAGCCCC 900 CACTCTGACC CCTTTACTCT GACCCCTTTA TTGTCTACTC CTCAGAGCCC CCAGTCTGTG 960 TCCTTCTAAC TTAGAAAGGG GATTATGGCT CAGAGTCCAA CTCTGTGCTC AGAGCTTTCA 1020 ACAACTACTC AGAAACACAA GATGCTGGGA CAGTGACCTG GACTGTGGGC CTCTCATGCA 1080 CCACCATCAA GGACTCAAAT GGGCTTTCCG AATTCACTGG AGCCTCGAAT GTCCATTCCT GAGTTCTGCA AAGGGAGAGT GGTCAGGTTG CCTCTGTCTC AGAATGAGGC TGGATAAGAT 1200 CTCAGGCCTT CCTACCTTCA GACCTTTCCA GACTCTTCCC TGAGGTGCAA TGCACAGCCT 1260 TCCTCACAGA GCCAGCCCCC CTCTATTTAT ATTTGCACTT ATTATTTATT ATTTATTTAT 1320 TATTTATTTA TTTGCTTATG AATGTATTTA TTTGGAAGGC CGGGGTGTCC TGGAGGACCC 1380 AGTGTGGGAA GCTGTCTTCA GACAGACATG TTTTCTGTGA AAACGGAGCT GAGCTGTCCC 1440 CACCTGGCCT CTCTACCTTG TTGCCTCCTC TTTTGCTTAT GTTTAAAACA AAATATTTAT 1500 CTAACCCAAT TGTCTTAATA ACGCTGATTT GGTGACCAGG CTGTCGCTAC ATCACTGAAC 1560

CTCTGCTCCC CACGGGAGCC GTGACTGTAA TTGCCCTACA GTCAATTGAG AGAAATAAAG 1620 ATCGCTTAAA ATAAAAAACC CCCC 1644

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1890 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AAACAGAGAG	AGATAGAGAA	AGAGAAAGAC	AGAGGTGTTT	CCCTTAGCTA	TGGAAACTCT	60
ATAAGAGAGA	TCCAGCTTGC	CTCCTCTTGA	GCAGTCAGCA	ACAGGGTCCC	GTCCTTGACA	120
CCTCAGCCTC	TACAGGACTG	AGAAGAAGTA	AAACCGTTTG	CTGGGGCTGG	CCTGACTCAC	180
CAGCTGCCAT	GCAGCAGCCC	TTCAATTACC	CATATCCCCA	GATCTACTGG	GTGGACAGCA	240
GTGCCAGCTC	TCCCTGGGCC	CCTCCAGGCA	CAGTTCTTCC	CTGTCCAACC	TCTGTGCCCA	300
GAAGGCCTGG	TCAAAGGAGG	CCACCACCAC	CACCGCCACC	GCCACCACTA	CCACCTCCGC	360
CGCCGCCGCC	ACCACTGCCT	CCACTACCGC	TGCCACCCCT	GAAGAAGAGA	GGGAACCACA	420
GCACAGGCCT	GTGTCTCCTT	GTGATGTTTT	TCATGGTTCT	GGTTGCCTTG	GTAGGATTGG	480
GCCTGGGGAT	GTTTCAGCTC	TTCCACCTAC	AGAAGGAGCT	GGCAGAACTC	CGAGAGTCTA	540
CCAGCCAGAT	GCACACAGCA	TCATCTTTGG	AGAAGCAAAT	AGGCCACCCC	AGTCCACCCC	600
CTGAAAAAAA	GGAGCTGAGG	AAAGTGGCCC	ATTTAACAGG	CAAGTCCAAC	TCAAGGTCCA	660
TGCCTCTGGA	ATGGGAAGAC	ACCTATGGAA	TTGTCCTGCT	TTCTGGAGTG	AAGTATAAGA	720
AGGGTGGCCT	TGTGATCAAT	GAAACTGGGC	TGTACTTTGT	ATATTCCAAA	GTATACTTCC	780
GGGGTCAATC	TTGCAACAAC	CTGCCCCTGA	GCCACAAGGT	CTACATGAGG	AACTCTAAGT	840
ATCCCCAGGA	TCTGGTGATG	ATGGAGGGGA	AGATGATGAG	CTACTGCACT	ACTGGGCAGA	900
TGTGGGCCCG	CAGCAGCTAC	CTGGGGGCAG	TGTTCAATCT	TACCAGTGCT	GATCATTTAT	960
ATGTCAACGT	ATCTGAGCTC	TCTCTGGTCA	ATTTTGAGGA	ATCTCAGACG	TTTTTCGGCT	1020
TATATAAGCT	CTAAGAGAAG	CACTTTGGGA	TTCTTTCCAT	TATGATTCTT	TGTTACAGGC	1080
ACCGAGAATG	TTGTATTCAG	TGAGGGTCTT	CTTACATGCA	TTTGAGGTCA	AGTAAGAAGA	1140
CATGAACCAA	GTGGACCTTG	AGACCACAGG	GTTCAAAATG	TCTGTAGCTC	CTCAACTCAC	1200
CTAATGTTTA	TGAGCCAGAC	AAATGGAGGA	ATATGACGGA	AGAACATAGA	ACTCTGGGCT	1260
GCCATGTGAA	GAGGGAGAAG	CATGAAAAAG	CAGCTACCCA	GGTGTTCTAC	ACTCATCTTA	1320
GTGCCTGAGA	GTATTTAGGC	AGATTGAAAA	GGACACCTTT	TAACTCACCT	CTCAAGGTGG	1380
GCCTTGCTAC	CTCAAGGGGG	ACTGTCTTTC	AGATACATGG	TTGTGACCTG	AGGATTTAAG	1440
GGATGGAAAA	GGAAGACTAG	AGGCTTGCAT	AATAAGCTAA	AGAGGCTGAA	AGAGGCCAAT	1500
GCCCCACTGG	CAGCATCTTC	ACTTCTAAAT	GCATATCCTG	AGCCATCGGT	GAAACTAACA	1560
GATAAGCAAG	AGAGATGTTT	TGGGGACTCA	TTTCATTCCT	AACACAGCAT	GTGTATTTCC	1620
AGTGCCAATT	GTAGGGGTGT	GTGTGTGTGT	GTGTGTGTGT	GTGTATGACT	AAAGAGAGAA	1680
TGTAGATATT	GTGAAGTACA	TATTAGGAAA	ATATGGGTTG	CATTTGGTCA	AGATTTTGAA	1740
TGCTTCCTGA	CAATCAACTC	TAATAGTGCT	TAAAAATCAT	TGATTGTCAG	CTACTAATGA	1800
TGTTTTCCTA	TAATATAATA	AATATTTATG	TAGATGTGCA	TTTTTGTGAA	ATGAAAACAT	1860
GTAATAAAAA	GTATATGTTA	GGATACAAAT				1890

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1541 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGGTGTCTCA	CAGAGAAGCA	AAGAGAAGAG	AACAGGAGAA	ATGGTGTTTC	CCTTGACTGC	60
GGAAACTTTA	TAAAGAAAAC	TTAGCTTCTC	TGGAGCAGTC	AGCGTCAGAG	TTCTGTCCTT	120
GACACCTGAG	TCTCCTCCAC	AAGGCTGTGA	GAAGGAAACC	CTTTCCTGGG	GCTGGGTGCC	180
ATGCAGCAGC	CCATGAATTA	CCCATGTCCC	CAGATCTTCT	GGGTAGACAG	CAGTGCCACT	240
TCATCTTGGG	CTCCTCCAGG	GTCAGTTTTT	CCCTGTCCAT	CTTGTGGGCC	TAGAGGGCCG	300
GACCAAAGGA	GACCGCCACC	TCCACCACCA	CCTGTGTCAC	CACTACCACC	GCCATCACAA	360
CCACTCCCAC	TGCCGCCACT	GACCCCTCTA	AAGAAGAAGG	ACCACAACAC	AAATCTGTGG	420
CTACCGGTGG	TATTTTTCAT	GGTTCTGGTG	GCTCTGGTTG	GAATGGGATT	AGGAATGTAT	480
CAGCTCTTCC	ACCTGCAGAA	GGAACTGGCA	GAACTCCGTG	AGTTCACCAA	CCAAAGCCTT	540
AAAGTATCAT	CTTTTGAAAA	GCAAATAGCC	AACCCCAGTA	CACCCTCTGA	AAAAAAAGAG	600
CCGAGGAGTG	TGGCCCATTT	AACAGGGAAC	CCCCACTCAA	GGTCCATCCC	TCTGGAATGG	660
GAAGACACAT	ATGGAACCGC	TCTGATCTCT	GGAGTGAAGT	ATAAGAAAGG	TGGCCTTGTG	720
ATCAACGAAA	CTGGGTTGTA	CTTCGTGTAT	TCCAAAGTAT	ACTTCCGGGG	TCAGTCTTGC	780
AACAACCAGC	CCCTAAACCA	CAAGGTCTAT	ATGAGGAACT	CTAAGTATCC	TGAGGATCTG	840
GTGCTAATGG	AGGAGAAGAG	GTTGAACTAC	TGCACTACTG	GCCAGATATG	GGCCCACAGC	900
AGCTACCTGG	GGGCAGTATT	CAATCTTACC	AGTGCTGACC	ATTTATATGT	CAACATATCT	960
CAACTCTCTC	TGATCAATTT	TGAGGAATCT	AAGACCTTTT	TCGGCTTGTA	TAAGCTTTAA	1020
AAGAAAAAGC	ATTTTAAAAT	GATCTACTAT	TCTTTATCAT	GGGCACCAGG	AATATTGTCT	1080
TGAATGAGAG	TCTTCTTAAG	ACCTATTGAG	ATTAATTAAG	ACTACATGAG	CCACAAAGAC	1140
CTCATGACCG	CAAGGTCCAA	CAGGTCAGCT	ATCCTTCATT	TTCTCGAGGT	CCATGGAGTG	1200
GTCCTTAATG	CCTGCATCAT	GAGCCAGATG	GAAGGAGGTC	TGTGACTGAG	GGACATAAAG	1260
CTTTGGGCTG	CTGTGTAGCA	ATGCAGAGGC	ACAGAGAAAG	AACTGTCTGA	TGTTAAATGG	1320
CCAAGAGAAT	TTTAACCATT	GAAGAAGACA	CCTTTACACT	CACTTCCAGG	GTGGGTCTAC	1380
TTACTACCTC	ACAGAGGCCG	TTTTTGAGAC	ATAGTTGTGG	TATGAATATA	CAAGGGTGAG	1440
AAAGGAGGCT	CATTTGACTG	ATAAGCTAGA	GACTGAAAAA	AAGACAGTGT	CTCATTGGCA	1500
CCATCTTTAC	TGTTACCTGA	TGTTTTCTGA	GCCGACCTTT	G		1541

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	888 base pairs
(B)	TYPE:	nucleic acid

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GGCTGGTCCC	CTGACAGGTT	GAAGCAAGTA	GACGCCCAGG	AGCCCCGGGA	GGGGGCTGCA	60
GTTTCCTTCC	TTCCTTCTCG	GCAGCGCTCC	GCGCCCCCAT	CGCCCCTCCT	GCGCTAGCGG	120
AGGTGATCGC	CGCGGCGATG	CCGGAGGAGG	GTTCGGGCTG	CTCGGTGCGG	CGCAGGCCCT	180
ATGGGTGCGT	CCTGCGGGCT	GCTTTGGTCC	CATTGGTCGC	GGGCTTGGTG	ATCTGCCTCG	240
TGGTGTGCAT	CCAGCGCTTC	GCACAGGCTC	AGCAGCAGCT	GCCGCTCGAG	TCACTTGGGT	300
GGGACGTAGC	TGAGCTGCAG	CTGAATCACA	CAGGACCTCA	GCAGGACCCC	AGGCTATACT	360
GGCAGGGGGG	CCCAGCACTG	GGCCGCTCCT	TCCTGCATGG	ACCAGAGCTG	GACAAGGGGC	420
AGCTACGTAT	CCATCGTGAT	GGCATCTACA	TGGTACACAT	CCAGGTGACG	CTGGCCATCT	480
GCTCCTCCAC	GACGGCCTCC	AGGCACCACC	CCACCACCCT	GGCCGTGGGA	ATCTGCTCTC	540
CCGCCTCCCG	TAGCATCAGC	CTGCTGCGTC	TCAGCTTCCA	CCAAGGTTGT	ACCATTGCCT	600
CCCAGCGCCT	GACGCCCCTG	GCCCGAGGGG	ACACACTCTG	CACCAACCTC	ACTGGGACAC	660
TTTTGCCTTC	CCGAAACACT	GATGAGACCT	TCTTTGGAGT	GCAGTGGGTG	CGCCCTGAC	720
CACTGCTGCT	GATTAGGGTT	TTTTAAATTT	TATTTTATTT	TATTTAAGTT	CAAGAGAAAA	780
AGTGTACACA	CAGGGGCCAC	CCGGGGTTGG	GGTGGGAGTG	TGGTGGGGG	TAGTGGTGGC	840
AGGACAAGAG	AAGGCATTGA	GCTTTTTCTT	TCATTTTCCT	ATTAAAAA		888

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1906 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CCAAGTCACA	TGATTCAGGA	TTCAGGGGGA	GAATCCTTCT	TGGAACAGAG	ATGGGCCCAG	60
AACTGAATCA	GATGAAGAGA	GATAAGGTGT	GATGTGGGGA	AGACTATATA	AAGAATGGAC	120
CCAGGGCTGC	AGCAAGCACT	CAACGGAATG	GCCCCTCCTG	GAGACACAGC	CATGCATGTG	180
CCGGCGGGCT	CCGTGGCCAG	CCACCTGGGG	ACCACGAGCC	GCAGCTATTT	CTATTTGACC	240
ACAGCCACTC	TGGCTCTGTG	CCTTGTCTTC	ACGGTGGCCA	CTATTATGGT	GTTGGTCGTT	300
CAGAGGACGG	ACTCCATTCC	CAACTCACCT	GACAACGTCC	CCCTCAAAGG	AGGAAATTGC	360
TCAGAAGACC	TCTTATGTAT	CCTGAAAAGA	GCTCCATTCA	AGAAGTCATG	GGCCTACCTC	420
CAAGTGGCAA	AGCATCTAAA	CAAAACCAAG	TTGTCTTGGA	ACAAAGATGG	CATTCTCCAT	480
GGAGTCAGAT	ATCAGGATGG	GAATCTGGTG	ATCCAATTCC	CTGGTTTGTA	CTTCATCATT	540
TGCCAACTGC	AGTTTCTTGT	ACAATGCCCA	AATAATTCTG	TCGATCTGAA	GTTGGAGCTT	600
CTCATCAACA	AGCATATCAA	AAAACAGGCC	CTGGTGACAG	TGTGTGAGTC	TGGAATGCAA	660
ACGAAACACG	TATACCAGAA	TCTCTCTCAA	TTCTTGCTGG	ATTACCTGCA	GGTCAACACC	720
ACCATATCAG	TCAATGTGGA	TACATTCCAG	TACATAGATA	CAAGCACCTT	TCCTCTTGAG	780
AATGTGTTGT	CCATCTTCTT	ATACAGTAAT	TCAGACTGAA	CAGTTTCTCT	TGGCCTTCAG	840
GAAGAAAGCG	CCTCTCTACC	ATACAGTATT	TCATCCCTCC	AAACACTTGG	GCAAAAAGAA	900
AACTTTAGAC	CAAGACAAAC	TACACAGGGT	ATTAAATAGT	ATACTTCTCC	TTCTGTCTCT	960
TGGAAAGATA	CAGCTCCAGG	GTTAAAAAGA	GAGTTTTTAG	TGAAGTATCT	TTCAGATAGC	1020
AGGCAGGGAA	GCAATGTAGT	GTGGTGGGCA	GAGCCCCACA	CAGAATCAGA	AGGGATGAAT	1080
	GCCCAACCAC	TAATTCACTG	TATGGTCTTG	ATCTATTTCT	TCTGTTTTGA	1140
GAGCCTCCAG	TTAAAATGGG	GCTTCAGTAC	CAGAGCAGCT	AGCAACTCTG	CCCTAATGGG	1200
AAATGAAGGG	GAGCTGGGTG	TGAGTGTTTA	CACTGTGCCC	TTCACGGGAT	ACTTCTTTTA	1260
TCTGCAGATG	GCCTAATGCT	TAGTTGTCCA	AGTCGCGATC	AAGGACTCTC	TCACACAGGA	1320
AACTTCCCTA	TACTGGCAGA	TACACTTGTG	ACTGAACCAT	GCCCAGTTTA	TGCCTGTCTG	1380
ACTGTCACTC		AGGCTGATCT	TGTACTCCAT	ATGACCCCAC	CCCTAGGAAC	1440
CCCCAGGGAA	AACCAGGCTC	GGACAGCCCC	CTGTTCCTGA	GATGGAAAGC	ACAAATTTAA	1500
		CAAGTTCAAA	GACTTTTACT	TACAGATCCT	GGACAGAAAG	1560
GGCATAATGA	GTCTGAAGGG	CAGTCCTCCT	TCTCCAGGTT	ACATGAGGCA	GGAATAAGAA	1620
		CAGTTAACAA			GTGGTCACTC	1680
		TGAATGGTCT		AGCAACAGAG	AAGTGGGGAA	1740
TCCAGTCTGC		AGATGCCTCT		CTCTGGCCAG	AGGTGTGGTA	1800
		AAGGGTGACT		TCCGGTATGA	GAAATTAAAC	1860
TTGTATACAA	AATGGTTGCC	AAGGCAACAT	AAAATTATAA	GAATTC		1906

(2) INFORMATION FOR SEQ ID NO: 17:

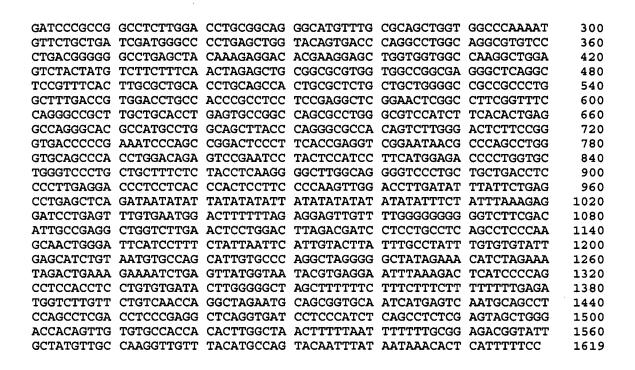
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1619 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GTCATGGAAT	ACGCCTCTGA	CGCTTCACTG	GACCCCGAAG	CCCCGTGGCC	TCCCGCGCCC	60
CGCGCTCGCG	CCTGCCGCGT	ACTGCCTTGG	GCCCTGGTCG	CGGGGCTGCT	GCTGCTGCTG	120
CTGCTCGCTG	CCGCCTGCGC	CGTCTTCCTC	GCCTGCCCCT	GGGCCGTGTC	CGGGGCTCGC	180
GCCTCGCCCG	GCTCCGCGGC	CAGCCCGAGA	CTCCGCGAGG	GTCCCGAGCT	TTCGCCCGAC	240



(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1239 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

AGCCTATAAA	GCACGGGCAC	TGGCGGGAGA	CGTGCACTGA	CCGACCGTGG	TAATGGACCA	60
GCACACACTT	GATGTGGAGG	ATACCGCGGA	TGCCAGACAT	CCAGCAGGTA	CTTCGTGCCC	120
CTCGGATGCG	GCGCTCCTCA	GAGATACCGG	GCTCCTCGCG	GACGCTGCGC	TCCTCTCAGA	180
TACTGTGCGC	CCCACAAATG	CCGCGCTCCC	CACGGATGCT	GCCTACCCTG	CGGTTAATGT	240
TCGGGATCGC	GAGGCCGCGT	GGCCGCCTGC	ACTGAACTTC	TGTTCCCGCC	ACCCAAAGCT	300
CTATGGCCTA	GTCGCTTTGG	TTTTGCTGCT	TCTGATCGCC	GCCTGTGTTC	CTATCTTCAC	360
CCGCACCGAG	CCTCGGCCAG	CGCTCACAAT	CACCACCTCG	CCCAACCTGG	GTACCCGAGA	420
GAATAATGCA	GACCAGGTCA	CCCCTGTTTC	CCACATTGGC	TGCCCCAACA	CTACACAACA	480
GGGCTCTCCT	${\tt GTGTTCGCCA}$	AGCTACTGGC	TAAAAACCAA	GCATCGTTGT	GCAATACAAC	540
TCTGAACTGG	CACAGCCAAG	ATGGAGCTGG	GAGCTCATAC	CTATCTCAAG	GTCTGAGGTA	600
CGAAGAAGAC	AAAAAGGAGT	TGGTGGTAGA	CAGTCCCGGG	CTCTACTACG	TATTTTTGGA	660
ACTGAAGCTC	AGTCCAACAT	TCACAAACAC	AGGCCACAAG	GTGCAGGGCT	GGGTCTCTCT	720
TGTTTTGCAA	GCAAAGCCTC	AGGTAGATGA	CTTTGACAAC	TTGGCCCTGA	CAGTGGAACT	780
GTTCCCTTGC	TCCATGGAGA	ACAAGTTAGT	GGACCGTTCC	TGGAGTCAAC	TGTTGCTCCT	840
GAAGGCTGGC	CACCGCCTCA	GTGTGGGTCT	GAGGGCTTAT	CTGCATGGAG	CCCAGGATGC	900
ATACAGAGAC	TGGGAGCTGT	CTTATCCCAA	CACCACCAGC	TTTGGACTCT	TTCTTGTGAA	960
ACCCGACAAC	CCATGGGAAT	GAGAACTATC	CTTCTTGTGA	CTCCTAGTTG	CTAAGTCCTC	1020
AAGCTGCTAT	GTTTTATGGG	GTCTGAGCAG	GGGTCCCTTC	CATGACTTTC	TCTTGTCTTT	1080
AACTGGACTT	GGTATTTATT	CTGAGCATAG	CTCAGACAAG	ACTTTATATA	ATTCACTAGA	1140
TAGCATTAGT	AAACTGCTGG	GCAGCTGCTA	GATAAAAAAA	AATTTCTAAA	TCAAAGTTTA	1200
TATTTATATT	AATATATAAA	AATAAATGTG	TTTGTAAAT			1239

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	606 base pairs
(B)	TYPE:	nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATGATCGAAA	CATACAACCA	AACTTCTCCC	CGATCTGCGG	CCACTGGACT	GCCCATCAGC	60
ATGAAAATTT	TTATGTATTT	ACTTACTGTT	TTTCTTATCA	CCCAGATGAT	TGGGTCAGCA	120
CTTTTTGCTG	TGTATCGCTT	CGCACAGGCT	TTTGAAATGC	AAAAAGGTGA	TCAGAATCCT	180
CAAATTGCGG	CACATGTCAT	AAGTGAGGCC	AGCAGTAAAA	CAACATCTGT	GTTACAGTGG	240
GCTGAAAAAG	GATACTACAC	CATGAGCAAC	AACTTGGTAA	CCCTGGAAAA	TGGGAAACAG	300
CTGACCGTTA	AAAGACAAGG	ACTCTATTAT	ATCTATGCCC	AAGTCACCTT	CTGTTCCAAT	360
CGGGAAGCTT	CGAGTCAAGC	TCCATTTATA	GCCAGCCTCT	GCCTAAAGTC	CCCCGGTAGA	420
TTCGAGAGAA	TCTTACTCAG	AGCTGCAAAT	ACCCACAGTT	CCGCCAAACC	TTGCGGGCAA	480
CAATCCATTC	ACTTGGGAGG	AGTATTTGAA	TTGCAACCAG	GTGCTTCGGT	GTTTGTCAAT	540
GTGACTGATC	CAAGCCAAGT	GAGCCATGGC	ACTGGCTTCA	CGTCCTTTGG	CTTACTCAAA	600
CTCTGA						606

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	783 base pairs
(B)	TYPE:	nucleic acid
(0)	COD SANDEDATE CO	-i1-

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ATGATCGAAA	CATACAACCA	AACTTCTCCC	CGATCTGCGG	CCACTGGACT	GCCCATCAGC	60
ATGAAAATTT	TTATGTATTT	ACTTACTGTT	TTTCTTATCA	CCCAGATGAT	TGGGTCAGCA	120
CTTTTTGCTG	TGTATCTTCA	TAGAAGATTG	GATAAGGTCG	AAGAGGAAGT	AAACCTTCAT	180
GAAGATTTTG	TATTCATAAA	AAAGCTAAAG	AGATGCAACA	AAGGAGAAGG	ATCTTTATCC	240
TTGCTGAACT	GTGAGGAGAT	GAGAAGGCAA	TTTGAAGACC	TTGTCAAGGA	TATAACGTTA	300
AACAAAGAAG	AGAAAAAAGA	AAACAGCTTT	GAAATGCAAA	AAGGTGATCA	GAATCCTCAA	360
ATTGCGGCAC	ATGTCATAAG	TGAGGCCAGC	AGTAAAACAA	CATCTGTGTT	ACAGTGGGCT	420
GAAAAAGGAT	ACTACACCAT	GAGCAACAAC	TTGGTAACCC	TGGAAAATGG	GAAACAGCTG	480
ACCGTTAAAA	GACAAGGACT	CTATTATATC	TATGCCCAAG	TCACCTTCTG	TTCCAATCGG	540
GAAGCTTCGA	GTCAAGCTCC	ATTTATAGCC	AGCCTCTGCC	TAAAGTCCCC	CGGTAGATTC	600
GAGAGAATCT	TACTCAGAGC	TGCAAATACC	CACAGTTCCG	CCAAACCTTG	CGGGCAACAA	660
TCCATTCACT	TGGGAGGAGT	ATTTGAATTG	CAACCAGGTG	CTTCGGTGTT	TGTCAATGTG	720
	GCCAAGTGAG	CCATGGCACT	GGCTTCACGT	CCTTTGGCTT	ACTCAAACTC	780
TGA						783

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	558 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS.	ginale

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CTGCTGCACT	TCGGGGTAAT	CGGCCCCCAG	AGGGAAGAGC	AGTCCCCAGG	TGGCCCCTCC	60
ATCAACAGCC	CTCTGGTTCA	AACACTCAGG	TCCTCTTCTC	AAGCCTCAAG	TAACAAGCCG	120
GTAGCCCACG	TTGTAGCCGA	CATCAACTCT	CCGGGGCAGC	TCCGGTGGTG	GGACTCGTAT	180
GCCAATGCCC	TCATGGCCAA	CGGTGTGAAG	CTGGAAGACA	ACCAGCTGGT	GGTGCCTGCT	240
GACGGGCTTT	ACCTCATCTA	CTCACAGGTC	CTCTTCAGGG	GCCAAGGCTG	CCCTTCCACC	300
CCCTTGTTCC	TCACCCACAC	CATCAGCCGC	ATTGCAGTCT	CCTACCAGAC	CAAGGTCAAC	360
ATCCTGTCTG	CCATCAAGAG	CCCTTGCCAC	AGGGAGACCC	CAGAGTGGGC	TGAGGCCAAG	420
CCCTGGTACG	AACCCATCTA	CCAGGGAGGA	GTCTTCCAGC	TGGAGAAGGG	AGATCGCCTC	480
AGTGCTGAGA	TCAACCTGCC	GGACTACCTG	GACTATGCCG	AGTCCGGGCA	GGTCTACTTT	540
GGGATCATTG	CCCTGTGA					558

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	1783 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TODOLOGY.	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CAAGTCACAT	GATCCAGGAT	GCAGGGGAAA	ATCCTTCTTG	GAACAGAGCT	GGGTACAGAA	60
CCGAATCAGA	TGAGGAGAGA	TAAGGTGTGA	TGTGGGACAG	ACTATATAAA	GCATGGAGCC	120
AGGGCTGCAA	CAAGCAGGCA	GCTGTGGGGC	TCCTTCCCCT	GACCCAGCCA	TGCAGGTGCA	180
GCCCGGCTCG	GTAGCCAGCC	CCTGGAGAAG	CACGAGGCCC	TGGAGAAGCA	CAAGTCGCAG	240
CTACTTCTAC	CTCAGCACCA	CCGCACTGGT	GTGCCTTGTT	GTGGCAGTGG	CGATCATTCT	300
GGTACTGGTA	GTCCAGAAAA	AGGACTCCAC	TCCAAATACA	ACTGAGAAGG	CCCCCTTAA	360
AGGAGGAAAT	TGCTCAGAGG	ATCTCTTCTG	TACCCTGAAA	AGTACTCCAT	CCAAGAAGTC	420
ATGGGCCTAC	CTCCAAGTGT	CAAAGCATCT	CAACAATACC	AAACTGTCAT	GGAACGAAGA	480
TGGCACCATC	CACGGACTCA	TATACCAGGA	CGGGAACCTG	ATAGTCCAAT	TCCCTGGCTT	540
GTACTTCATC	GTTTGCCAAC	TGCAGTTCCT	CGTGCAGTGC	TCAAATCATT	CTGTGGACCT	600
GACATTGCAG	CTCCTCATCA	ATTCCAAGAT	CAAAAAGCAG	ACGTTGGTAA	CAGTGTGTGA	660
GTCTGGAGTT	CAGAGTAAGA	ACATCTACCA	GAATCTCTCT	CAGTTTTTGC	TGCATTACTT	720
ACAGGTCAAC	TCTACCATAT	CAGTCAGGGT	GGATAATTTC	CAGTATGTGG	ATACAAACAC	780
TTTCCCTCTT	GATAATGTGC	TATCCGTCTT	CTTATATAGT	AGCTCAGACT	GAATAGTTGT	840
TCTTAACCTT	TATGAAAATG	CTGTCTACCA	TACAGTACTT	CATCTGTCCA	AACATGGGCC	900
AAAGAAAATA	TTAGGACAAC	TCAAACTAAG	CATGTGAGTT	AGTGCACTTC	TCTTTCTGTC	960
CTTTGGAAAA	ATACAAACCC	AGGATTTAGA	AAGTGGAGTC	TCCTTCAGAT	GCACAAACAG	1020
GAAAGAATGT	GATATGTGCA	CAGAGACCTA	CTTGGGCACT	AGAAGGGGTG	TGAGTTGTCC	1080
CAGTATAACC	ACTAATTCAC	TGACCTTGAG	CCATTTTTCC	TTCCCCCTGG	AACTTGGGGT	1140
CTGAATCTGG	AAAAGTAGGA	GATGAGATTT	ACATTTCCCC	AATATTTTCT	TCAACTCAGA	1200
AGACGAGACT	GTGGAGCTGA	GCTCCCTACA	CAGATGAAGG	CCTCCCATGG	CATGAGGAAA	1260
ATGATGGTAC	CAGTAATGTC	TGTCTGACTG	TCATCTCAGC	AAGTCCTAAG	GACTTCCATG	1320
CTGCCTTGTT	GAAAGATACT	CTAACCTCTT	GTAATGGGCA	AAGTGATCCT	GTCTCTCACT	1380
GAGGGGAGTA	GCTGCTGCCA	TCTCCTGAGA	CATACATGGA	GACATTTTCT	GCCCAAATTC	1440
CATTCTGTGT	GCAGTTTTTA	AGTATTCCCC	CAAAAGTTCT	TGACAATGAG	AACTTTGAAT	1500
GTGGGAAGAG	CTTCTGGACA	GCAAACATTA	ACAGCTTCTC	CTGACCAGAG	AGACCATGCA	1560
AGCTTGGTCT	TAGACCCATC	AAGCTTGAGG	TTTCTACATT	GTGGGAGACA	GACTTTTGAC	1620
AAACCATTTG	AGTTGATGTC	TGGGCCCCTG	GGAGTTCTCC	TTCAGTAAGG	AGAGCAAGCC	1680
GTTCTAGTGC	TGTGTCAGAG	GATGGAGTAA	AATAGACACT	TTTCTGAAGG	AAAGGAGAAC	1740
AAAGTTCCAG	AAAAAGGCTA	GAAAATGTTT	AAAAAGAAAA	AAA		1783

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1047 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AGAGAGCGCT GGGAGCCGGA GGGGAGCGCA GCGAGTTTTG GCCAGTGGTC GTGCAGTCCA	60
AGGGGCTGGA TGGCATGCTG GACCCAAGCT CAGCTCAGCG TCCGGACCCA ATAACAGTTT	120
TACCAAGGGA GCAGCTTTCT ATCCTGGCCA CACTGAGGTG CATAGCGTAA TGTCCATGTT	180
GTTCTACACT CTGATCACAG CTTTTCTGAT CGGCATACAG GCGGAACCAC ACTCAGAGAG	240
CAATGTCCCT GCAGGACACA CCATCCCCCA AGTCCACTGG ACTAAACTTC AGCATTCCCT	300
TGACACTGCC CTTCGCAGAG CCCGCAGCGC CCCGGCAGCG GCGATAGCTG CACGCGTGGC	360
GGGGCAGACC CGCAACATTA CTGTGGACCC CAGGCTGTTT AAAAAGCGGC GACTCCGTTC	420
ACCCCGTGTG CTGTTTAGCA CCCAGCCTCC CCGTGAAGCT GCAGACACTC AGGATCTGGA	480
CTTCGAGGTC GGTGGTGCTG CCCCCTTCAA CAGGACTCAC AGGAGCAAGC GGTCATCATC	540
CCATCCCATC TTCCACAGGG GCGAATTCTC GGTGTGTGAC AGTGTCAGCG TGTGGGTTGG	600
GGATAAGACC ACCGCCACAG ACATCAAGGG CAAGGAGGTG ATGGTGTTGG GAGAGGTGAA	660
CATTAACAAC AGTGTATTCA AACAGTACTT TTTTGAGACC AAGTGCCGGG ACCCAAATCC	720
CGTTGACAGC GGGTGCCGGG GCATTGACTC AAAGCACTGG AACTCATATT GTACCACGAC	780
TCACACCTTT GTCAAGGCGC TGACCATGGA TGGCAAGCAG GCTGCCTGGC GGTTTATCCG	840
GATAGATACG GCCTGTGTGT GTGTGCTCAG CAGGAAGGCT GTGAGAAGAG CCTGACCTGC	900
CGACACGCTC CCTCCCCTG CCCCTTCTAC ACTCTCCTGG GCCCCTCCCT ACCTCAACCT	960
GTAAATTATT TTAAATTATA AGGACTGCAT GGTAATTTAT AGTTTATACA GTTTTAAAGA 1	.020
ATCATTATTT ATTAAATTTT TGGAAGC	.047

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GAGCGCCTGG	AGCCGGAGGG	GAGCGCATCG	AGTGACTTTG	GAGCTGGCCT	TATATTTGGA	60
TCTCCCGGGC	AGCTTTTTGG	AAACTCCTAG	TGAACATGCT	GTGCCTCAAG	CCAGTGAAAT	120
TAGGCTCCCT	GGAGGTGGGA	CACGGGCAGC	ATGGTGGAGT	TTTGGCCTGT	GGTCGTGCAG	180
TCCAGGGGGC	TGGATGGCAT	GCTGGACCCA	AGCTCACCTC	AGTGTCTGGG	CCCAATAAAG	240
GTTTTGCCAA	GGACGCAGCT	TTCTATACTG	GCCGCAGTGA	GGTGCATAGC	GTAATGTCCA	300
TGTTGTTCTA	CACTCTGATC	ACTGCGTTTT	TGATCGGCGT	ACAGGCAGAA	CCGTACACAG	360
ATAGCAATGT	CCCAGAAGGA	GACTCTGTCC	CTGAAGCCCA	CTGGACTAAA	CTTCAGCATT	420
CCCTTGACAC	AGCCCTCCGC	AGAGCCCGCA	GTGCCCCTAC	TGCACCAATA	GCTGCCCGAG	480
TGACAGGGCA	GACCCGCAAC	ATCACTGTAG	ACCCCAGACT	GTTTAAGAAA	CGGAGACTCC	540
ACTCACCCCG	TGTGCTGTTC	AGCACCCAGC	CTCCACCCAC	CTCTTCAGAC	ACTCTGGATC	600
TAGACTTCCA	GGCCCATGGT	ACAATCCCTT	TCAACAGGAC	TCACCGGAGC	AAGCGCTCAT	660
CCACCCACCC	AGTCTTCCAC	ATGGGGGAGT	TCTCAGTGTG	TGACAGTGTC	AGTGTGTGGG	720
TTGGAGATAA	GACCACAGCC	ACAGACATCA	AGGGCAAGGA	GGTGACAGTG	CTGGCCGAGG	780
TGAACATTAA	CAACAGTGTA	TTCAGACAGT	ACTTTTTTGA	GACCAAGTGC	CGAGCCTCCA	840
ATCCTGTTGA	GAGTGGGTGC	CGGGGCATCG	ACTCCAAACA	CTGGAACTCA	TACTGCACCA	900
CGACTCACAC	CTTCGTCAAG	GCGTTGACAA	CAGATGAGAA	GCAGGCTGCC	TGGAGGTTCA	960
TCCGGATAGA	CACAGCCTGT	GTGTGTGTGC	TCAGCAGGAA	GGCTACAAGA	AGAGGCTGAC	1020

TTGCCTGCAG CCCCCTTCCC CACCTGCCCC CTCCACACTC TCTTGGGCCC CTCCCTACCT 1080
CAGCCTGTAA ATTATTTAA ATTATAAGGA CTGCATGATA ATTATCGTT TATACAATTT 1140
TAAAGACATT ATTTATAAA TTTTCAAAGC ATCCTG 1176

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	1623 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TCAGAGTCCT	GTCCTTGACA	CTTCAGTCTC	CACAAGACTG	AGAGGAGGAA	ACCCTTTCCT	60
GGGGCTGGGT	GCCATGCAGC	AGCCCGTGAA	TTACCCATGT	CCCCAGATCT	ACTGGGTAGA	120
CAGCAGTGCC	ACTTCTCCTT	GGGCTCCTCC	AGGGTCAGTT	TTTTCTTGTC	CATCCTCTGG	180
GCCTAGAGGG	CCAGGACAAA	GGAGACCACC	GCCTCCACCA	CCACCTCCAT	CACCACTACC	240
ACCGCCTTCC	CAACCACCCC	CGCTGCCTCC	ACTAAGCCCT	CTAAAGAAGA	AGGACAACAT	300
AGAGCTGTGG	CTACCGGTGA	TATTTTTCAT	GGTGCTGGTG	GCTCTGGTTG	GAATGGGGTT	360
AGGAATGTAT	CAACTCTTTC	ATCTACAGAA	GGAACTGGCA	GAACTCCGTG	AGTTCACCAA	420
CCACAGCCTT	AGAGTATCAT	CTTTTGAAAA	GCAAATAGCC	AACCCCAGCA	CACCCTCTGA	480
AACCAAAAAG	CCAAGGAGTG	TGGCCCACTT	AACAGGGAAC	CCCCGCTCAA	GGTCCATCCC	540
TCTGGAATGG	GAAGACACAT	ATGGAACTGC	TTTGATCTCT	GGAGTGAAGT	ATAAGAAAGG	600
CGGCCTTGTG	ATCAATGAGG	CTGGGTTGTA	CTTCGTATAT	TCCAAAGTAT	ACTTCCGGGG	660
TCAGTCTTGC	AACAGCCAGC	CCCTAAGCCA	CAAGGTCTAT	ATGAGGAACT	TTAAGTATCC	720
TGGGGATCTG	GTGCTAATGG	AGGAGAAGAA	GTTGAATTAC	TGCACTACTG	GCCAGATATG	780
GGCCCACAGC	AGCTACCTAG	GGGCAGTATT	TAATCTTACC	GTTGCTGACC	ATTTATATGT	840
CAACATATCT	CAACTCTCTC	TGATCAATTT	TGAGGAATCT	AAGACCTTTT	TTGGCTTATA	900
TAAGCTTTAA	AGGAAAAAGC	ATTTTAGAAT	GATCTATTAT	TCTTTATCAT	GGATGCCAGG	960
AATATTGTCT	TCAATGAGAG	TCTTCTTAAG	ACCAATTGAG	CCACAAAGAC	CACAAGGTCC	1020
AACAGGTCAG	CTACCCTTCA	TTTTCTAGAG	GTCCATGGAG	TGGTCCTTAA	TGCCTGCATC	1080
ATGAGCCAGA	TGGGAAGAAG	ACTGTTCCTG	AGGAACATAA	AGTTTTGGGC	TGCTGTGTGG	1140
CAATGCAGAG	GCAAAGAGAA	GGAACTGTCT	GATGTTAAAT	GGCCAAGAGC	ATTTTAGCCA	1200
TTGAAGAAAA	AAAAAACCTT	TAAACTCACC	TTCCAGGGTG	GGTCTACTTG	CTACCTCACA	1260
GGAGGCCGTC	TTTTAGACAC	ATGGTTGTGG	TATGACTATA	CAAGGGTGAG	AAAGGATGCT	1320
AGGTTTCATG	GATAAGCTAG	AGACTGAAAA	AAGCCAGTGT	CCCATTGGCA	TCATCTTTAT	1380
TTTTAACTGA	TGTTTTCTGA	GCCCACCTTT	GATGCTAACA	GAGAAATAAG	AGGGGTGTTT	1440
GAGGCACAAG	TCATTCTCTA	CATAGCATGT	GTACCTCCAG	TGCAATGATG	TCTGTGTGTG	1500
TTTTTATGTA	TGAGAGTAGA	GCGATTCTAA	AGAGTCACAT	GAGTACAACG	CGTACATTAC	1560
GGAGTACATA	TTAGAAACGT	ATGTGTTACA	TTTGATGCTA	GAATATCTGA	ATGTTTCTTG	1620
CTA						1623

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	28 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

	,	
(2) IN	NFORMATION FOR SEQ ID NO: 27:	
(i	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi	i) SEQUENCE DESCRIPTION: SEQ ID NO: 27:	
GTTTCT	FAGAT CAGAGTTTGA GTAAGCC	27
(2) IN	NFORMATION FOR SEQ ID NO: 28:	
(i	i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi	i) SEQUENCE DESCRIPTION: SEQ ID NO: 28:	
CCAAGAC	CTAG TTAACACAGC ATGATCGAAA	30
(2) IN	NFORMATION FOR SEQ ID NO: 29:	
(i	i) SEQUENCE CHARACTERISTICS:	,
	(A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi	i) SEQUENCE DESCRIPTION: SEQ ID NO: 29:	
CCAATGC	CGGC CGCACTCAGA ATTCAACCTG	30
(2) IN	NFORMATION FOR SEQ ID NO: 30:	
(i	i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 972 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi	i) SEQUENCE DESCRIPTION: SEQ ID NO: 30:	
TGCCATG	CTCA GGACTGAGAA GAAGTAAAAC CGTTTGCTGG GGCTGGCCTG ACTCACCA GCAG CAGCCCTTCA ATTACCCATA TCCCCAGATC TACTGGGTGG ACAGCAGT TCCC TGGGCCCCTC CAGGCACAGT TCTTCCCTGT CCAACCTCTG TGCCCAGA	GC 120

GCCTGGTCAA	AGGAGGCCAC	CACCACCACC	GCCACCGCCA	CCACTACCAC	CTCCGCCGCC	240
GCCGCCACCA	CTGCCTCCAC	TACCGCTGCC	ACCCCTGAAG	AAGAGAGGGA	ACCACAGCAC	300
AGGCCTGTGT	CTCCTTGTGA	TGTTTTTCAT	GGTTCTGGTT	GCCTTGGTAG	GATTGGGCCT	360
GGGGATGTTT	CAGCTCTTCC	ACCTACAGAA	GGAGCTGGCA	GAACTCCGAG	AGTCTACCAG	420
CCAGATGCAC	ACAGCATCAT	CTTTGGAGAA	GCAAATAGGC	CACCCCAGTC	CACCCCTGA	480
AAAAAAGGAG	CTGAGGAAAG	TGGCCCATTT	AACAGGCAAG	TCCAACTCAA	GGTCCATGCC	540
TCTGGAATGG	GAAGACACCT	ATGGAATTGT	CCTGCTTTCT	GGAGTGAAGT	ATAAGAAGGG	600
TGGCCTTGTG	ATCAATGAAA	CTGGGCTGTA	CTTTGTATAT	TCCAAAGTAT	ACTTCCGGGG	660
TCAATCTTGC	AACAACCTGC	CCCTGAGCCA	CAAGGTCTAC	ATGAGGAACT	CTAAGTATCC	720
CCAGGATCTG	GTGATGATGG	AGGGGAAGAT	GATGAGCTAC	TGCACTACTG	GGCAGATGTG	780
GGCCCGCAGC	AGCTACCTGG	GGGCAGTGTT	CAATCTTACC	AGTGCTGATC	ATTTATATGT	840
CAACGTATCT	GAGCTCTCTC	TGGTCAATTT	TGAGGAATCT	CAGACGTTTT	TCGGCTTATA	900
TAAGCTCTAA	GAGAAGCACT	TTGGGATTCT	TTCCATTATG	ATTCTTTGTT	ACAGGCACCG	960
AGATGTTCTA	GA					972

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 885 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATGCAGCAGC	CCATGAATTA	CCCATGTCCC	CAGATCTTCT	GGGTAGACAG	CAGTGCCACT	60
TCATCTTGGG	CTCCTCCAGG	GTCAGTTTTT	CCCTGTCCAT	CTTGTGGGCC	TAGAGGGCCG	120
GACCAAAGGA	GACCGCCACC	TCCACCACCA	CCTGTGTCAC	CACTACCACC	GCCATCACAA	180
CCACTCCCAC	TGCCGCCACT	GACCCCTCTA	AAGAAGAAGG	ACCACAACAC	AAATCTGTGG	240
CTACCGGTGG	TATTTTTCAT	GGTTCTGGTG	GCTCTGGTTG	GAATGGGATT	AGGAATGTAT	300
CAGCTCTTCC	ACCTGCAGAA	GGAACTGGCA	GAACTCCGTG	AGTTCACCAA	CCAAAGCCTT	360
AAAGTATCAT	CTTTTGAAAA	GCAAATAGCC	AACCCCAGTA	CACCCTCTGA	AAAAAAAGAG	420
CCGAGGAGTG	TGGCCCATTT	AACAGGGAAC	CCCCACTCAA	GGTCCATCCC	TCTGGAATGG	480
GAAGACACAT	ATGGAACCGC	TCTGATCTCT	GGAGTGAAGT	ATAAGAAAGG	TGGCCTTGTG	540
ATCAACGAAG	CTGGGTTGTA	CTTCGTATAT	TCCAAAGTAT	ACTTCCGGGG	TCAGTCTTGC	600
AACAACCAGC	CCCTAAACCA	CAAGGTCTAT	ATGAGGAACT	CTAAGTATCC	TGGGGATCTG	660
GTGCTAATGG	AGGAGAAGAG	GTTGAACTAC	TGCACTACTG	GACAGATATG	GGCCCACAGC	720
AGCTACCTGG	GGGCAGTATT	CAATCTTACC	AGTGCTGACC	ATTTATATGT	CAACATATCT	780
CAACTCTCTC	TGATCAATTT	TGAGGAATCT	AAGACCTTTT	TCGGCTTGTA	TAAGCTTTAA	840
AAGAAAAAGC	ATTTTAAAAT	GATCTACTAT	TCTTTATCAT	GGGCA		885

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	29 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

	(X1)	SEQUENCE DESCRIPTION: SEQ 1D NO: 32:	
CTTA	AGCTT(C TACAGGACTG AGAAGAAGT	29
(2)	TMEO	DWARTON FOR GRO TO NO. 22	
(2)		RMATION FOR SEQ ID NO: 33:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 33:	
CTT	GAATT	CC AACATTCTCG GTGCCTGTAA	30
(2)	INFO	RMATION FOR SEQ ID NO: 34:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 34:	
TCI	AGGATC	CA CAAGGCTGTG AGAAGGA	27
(2)	INFO	RMATION FOR SEQ ID NO: 35:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 35:	
CTT	rgtcta	GA CCTGGTGCCC ATGATA	26

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	680 base pairs
(B)	TYPE:	nucleic acid

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

ATGCCGGAGG	AAGGTCGCCC	TTGCCCCTGG	GTTCGCTGGA	GCGGGACCGC	GTTCCAGCGC	60
CAATGGCCAT	GGCTGCTGCT	GGTGGTGTTT	ATTACTGTGT	TTTGCTGTTG	GTTTCATTGT	120
AGCGGACTAC	TCAGTAAGCA	GCAACAGAGG	CTGCTGGAGC	ACCCTGAGCC	GCACACAGCT	180
GAGTTACAGC	TGAATCTCAC	AGTTCCTCGG	AAGGACCCCA	CACTGCGCTG	GGGAGCAGGC	240
CCAGCCTTGG	GAAGGTCCTT	CACACACGGA	CCAGAGCTGG	AGGAGGGCCA	TCTGCGTATC	300
CATCAAGATG	GCCTCTACAG	GCTGCATATC	CAGGTGACAC	TGGCCAACTG	CTCTTCCCCA	360
GGCAGCACCC	TGCAGCACAG	GGCCACCCTG	GCTGTGGGCA	TCTGCTCCCC	CGCTGCGCAC	420
GGCATCAGCT	TGCTGCGTGG	GCGCTTTGGA	CAGGACTGTA	CAGTGGCATT	ACAGCGCCTG	480
ACATACCTGG	TCCACGGAGA	TGTCCTCTGT	ACCAACCTCA	CCCTGCCTCT	GCTGCCGTCC	540
CGCAACGCTG	ATGAGACCTT	CTTTGGAGTT	CAGTGGATAT	GCCCTTGACC	ACAACTCCAG	600
GATGACTTGT	GAATATTTTT	TTTCTTTTCA	AGTTCTACGT	ATTTATAAAT	GTATATAGTA	660
CACATAAAAA	AAAAAAAAA					680

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	846 base pairs
(B)	TYPE:	nucleic acid

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ATGCAGCAGC	CCTTCAATTA	CCCATATCCC	CAGATCTACT	GGGTGGACAG	CAGTGCCAGC	60
TCTCCCTGGG	CCCCTCCAGG	CACAGTTCTT	CCCTGTCCAA	CCTCTGTGCC	CAGAAGGCCT	120
GGTCAAAGGA	GGCCACCACC	ACCACCGCCA	CCGCCACCAC	TACCACCTCC	GCCGCCGCCG	180
CCACCACTGC	CTCCACTACC	GCTGCCACCC	CTGAAGAAGA	GAGGGAACCA	CAGCACAGGC	240
CTGTGTCTCC	TTGTGATGTT	TTTCATGGTT	CTGGTTGCCT	TGGTAGGATT	GGGCCTGGGG	300
ATGTTTCAGC	TCTTCCACCT	GCAGAAGGAA	CTGGCAGAAC	TCCGTGAGTT	CACCAACCAA	360
AGCCTTAAAG	TATCATCTTT	TGAAAAGCAA	ATAGGCCACC	CCAGTCCACC	CCCTGAAAAA	420
AAGGAGCTGA	GGAAAGTGGC	CCATTTAACA	GGCAAGTCCA	ACTCAAGGTC	CATGCCTCTG	480
GAATGGGAAG	ACACCTATGG	AATTGTCCTG	CTTTCTGGAG	TGAAGTATAA	GAAGGGTGGC	540
CTTGTGATCA	ATGAAACTGG	GCTGTACTTT	GTATATTCCA	AAGTATACTT	CCGGGGTCAA	600
TCTTGCAACA	ACCTGCCCCT	GAGCCACAAG	GTCTACATGA	GGAACTCTAA	GTATCCCCAG	660
GATCTGGTGA	TGATGGAGGG	GAAGATGATG	AGCTACTGCA	CTACTGGGCA	GATGTGGGCC	720
CGCAGCAGCT	ACCTGGGGGC	AGTGTTCAAT	CTTACCAGTG	CTGATCATTT	ATATGTCAAC	780
GTATCTGAGC	TCTCTCTGGT	CAATTTTGAG	GAATCTCAGA	CGTTTTTCGG	CTTATATAAG	840
CTCTAA						846

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	786 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

ATGCAGCAGC	CCTTCAATTA	CCCATATCCC	CAGATCTACT	GGGTGGACAG	CAGTGCCAGC	60
TCTCCCTGGG	CCCCTCCAGG	CACAGTTCTT	CCCTGTCCAA	CCTCTGTGCC	CAGAAGGCCT	120
GGTCAAAGGA	GGCCACCACC	ACCACCGCCA	CCGCCACCAC	TACCACCTCC	GCCGCCGCCG	180
			CTGAAGAAGA			240
CTGTGTCTCC	TTGTGATGTT	TTTCATGGTT	CTGGTTGCCT	TGGTAGGATT	GGGCCTGGGG	300
			ATAGGCCACC			360
			GGCAAGTCCA			420
			CTTTCTGGAG			
						480
CTTGTGATCA	ATGAAACTGG	GCTGTACTTT	GTATATTCCA	AAGTATACTT	CCGGGGTCAA	540
TCTTGCAACA	ACCTGCCCCT	GAGCCACAAG	GTCTACATGA	GGAACTCTAA	GTATCCCCAG	600
GATCTGGTGA	TGATGGAGGG	GAAGATGATG	AGCTACTGCA	CTACTGGGCA	GATGTGGGCC	660
CGCAGCAGCT	ACCTGGGGGC	AGTGTTCAAT	CTTACCAGTG	CTGATCATTT	ΔΤΑΤΩΤΟΔΑΟ	720
CTATIOTICACO	THE CHARGE COM	Ch a mmmma a c	23.3.000.000		MINI OI CARC	. – •
	TCTCTCTGGT	CAATTTTGAG	GAATCTCAGA	CGTTTTTCGG	CTTATATAAG	780
CTCTAA						786
						. • •

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	864 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

ATGCAGCAGC	CCTTCAATTA	CCCATATCCC	CAGATCTACT	GGGTGGACAG	CAGTGCCAGC	60
			CCCTGTCCAA			120
			CCGCCACCAC			180
CCACCACTGC	CTCCACTACC	GCTGCCACCC	CTGAAGAAGA	GAGGGAACCA	CAGCACAGGC	240
			CTGGTTGCCT			300
ATGTTTCAGC	TCTTCCAATC		CCCTATGCCG			360
GGTGCGGCGC	AGGCCCTATG	GGTGCGTCCT	GCGGCCATCC	TCAATCCTAT	AGGCCACCC	420
AGTCCACCCC	CTGAAAAAA	GGAGCTGAGG	AAAGTGGCCC	ATTTAACAGG	CAAGTCCAAC	480
TCAAGGTCCA	TGCCTCTGGA	ATGGGAAGAC	ACCTATGGAA	TTGTCCTGCT	TTCTGGAGTG	540
AAGTATAAGA	AGGGTGGCCT	TGTGATCAAT	GAAACTGGGC	TGTACTTTGT	ATATTCCAAA	600
GTATACTTCC	GGGGTCAATC	TTGCAACAAC	CTGCCCCTGA	GCCACAAGGT	CTACATGAGG	660
			ATGGAGGGGA			720
ACTGGGCAGA	TGTGGGCCCG	CAGCAGCTAC	CTGGGGGCAG	TGTTCAATCT	TACCAGTGCT	780
			TCTCTGGTCA			840
	TATATAAGCT					864
						004

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	828 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single

(D) TOPOLOGY: single linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

ATGCAGCAGC	CCTTCAATTA	CCCATATCCC	CAGATCTACT	GGGTGGACAG	CAGTGCCAGC	60
TCTCCCTGGG	CCCCTCCAGG	CACAGTTCTT	CCCTGTCCAA	CCTCTCTCCC	CACTACCAGC	
GGTCAAAGGA	GGCCACCACC	ACCACCGCCA	CCGCCACCAC	TRACE CONTRACT	CAGAAGGCCT	120
CCACCACTICA	OTTO CAROLAGO	ACCACCGCCA	CCGCCACCAC	TACCACCTCC	GCCGCCGCCG	180
CCACCACIGC	CTCCACTACC	GCTGCCACCC	CTGAAGAAGA	GAGGGAACCA	CAGCACAGGC	240
CTGTGTCTCC	TTGTGATGTT	TTTCATGGTT	CTGGTTGCCT	TGGTAGGATT	GGGCCTGGGG	300
ATGTTTCAGC	TCTTCCACCT	ACAGCGAGAG	TCTACCAGCC	AGATGCACAC	AGCATCATCT	360
TTGGAGAAGC	AAATAGGCCA	CCCCAGTCCA	CCCCTGAAA	AAAAGGAGCT	CACCAAACTC	420
GCCCATTTAA	CAGGCAAGTC	CAACTCAAGG	TCCATGCCTC	TOON A TOOM	DIDMANDONO	•
CCAAmmamaa	MCCMBmcmcc	CARCICARGG	TCCATGCCTC	TGGAATGGGA	AGACACCTAT	480
GGAATTGTCC	TGCTTTCTGG	AGTGAAGTAT	AAGAAGGGTG	GCCTTGTGAT	CAATGAAACT	540
GGGCTGTACT	TTGTATATTC	CAAAGTATAC	TTCCGGGGTC	AATCTTGCAA	CAACCTGCCC	600
CTGAGCCACA	AGGTCTACAT	GAGGAACTCT	AAGTATCCCC	AGGATCTGGT	CATCATCCAC	660
GGGAAGATGA	TGAGCTACTG	СУСТУСТССС	CAGATGTGGG	CCCCCTCTCCT	CELCATOOAG	
CCACMCMMCA	AMORMAGA	CACIACIGG	CAGAIGIGGG	CCCGCAGCAG	CTACCTGGGG	720
GCAGIGITCA	ATCTTACCAG	TGCTGATCAT	TTATATGTCA	ACGTATCTGA	GCTCTCTCTG	780
GTCAATTTTG	AGGAATCTCA	GACGTTTTTC	GGCTTATATA	AGCTCTAA		828
				·		020

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	846 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATGGCTATGA	$TGG\DeltaGGTCC\Delta$	GGGGGGAACCC	ACCOMOCOAA	NON COMOCOM	CCEC	
A MODERATOR	TOCAUGICCA	GGGGGGACCC	AGCCTGGGAC	AGACCTGCGT	GCTGATCGTG	60
ATCTTCACAG	TGCTCCTGCA	GTCTCTCTGT	GTGGCTGTAA	CTTACGTGTA	CTTTACCAAC	120
GAGCTGAAGC	AGATGCAGGA	CAAGTACTCC	AAAAGTGGCA	Ա ԱՐԱՆ ԱՄԵՐ ԱՄԵՐ ԱՄԵՐ ԱՄԵՐ ԱՄԵՐ ԱՄԵՐ ԱՄԵՐ ԱՄԵՐ	רדים א א א מא א א א א א א א א א א א א א א א	_ -
GATGACAGTT	ATTGGGACCC	CAATCACCAA	GAGAGTATGA	y Cy Cacacana	CTIMANUAA	180
33CECCC333C	Magamas age	CANTONCOM	GAGAGIAIGA	ACAGCCCCTG	CTGGCAAGTC	240
AAGTGGCAAC	TCCGTCAGCT	CGTTAGAAAG	ATGATTTTGA	GAACCTCTGA	GGAAACCATT	300
TCTACAGTTC	AAGAAAAGCA	ACAAAATATT	TCTCCCCTAG	TGAGAGAAAG	AGGTCCTCAG	360
AGAGTAGCAG	CTCACATAAC	TGGGACCAGA	GGAAGAAGCA	y Cy Cy mmcmc	TTCCTCCTCAC	
TOO A A O A A DO	333300000	TOUGHCCAGA	GGAAGAAGCA	ACACATTGTC	TTCTCCAAAC	420
TCCAAGAATG	AAAAGGCTCT	GGGCCGCAAA	ATAAACTCCT	GGGAATCATC	AAGGAGTGGG	480
CATTCATTCC	TGAGCAACTT	GCACTTGAGG	AATGGTGAAC	TGGTCATCCA	TGAAAAAGGG	540
TTTTACTACA	TCTATTCCCA	ልልሮልጥልሮ ጥጥጥ	CGATTTCAGG	70077770777	303333000	
7707700707	3363330000	MCATACITI	CGATTICAGG	AGGAAATAAA	AGAAAACACA	600
AAGAACGACA	AACAAATGGT	CCAATATATT	TACAAATACA	CAAGTTATCC	TGACCCTATA	660
TTGTTGATGA	AAAGTGCTAG	AAATAGTTGT	TGGTCTAAAG	ATGCAGAATA	ጥርርልርጥርጥልጥ	720
TCCATCTATC	AAGGGGGAAT	አጥጥጥር አርርጥጥ	AAGGAAAATG	303033555	TOURCICIAI	
10111011110	AMOUGUGAAI	ATTIGAGCTT	AAGGAAAATG	ACAGAATTTT	TGTTTCTGTA	780
ACAAATGAGC	ACTTGATAGA	CATGGACCAT	GAAGCCAGTT	TTTTCGGGGC	CTTTTTAGTT	840
GGCTAA				_	-	
						846

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	876 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

ATGCCTTCCT	CAGGGGCCCT	GAAGGACCTC	AGCTTCAGTC	AGCACTTCAG	CATCATCOTO	C 0
ΔͲͲͲϹϹϪͲϪϹ						60
			CAGGCTGTGT	CTGTGGCTGT	GACTTACATG	120
TACTTCACCA	ACGAGATGAA	GCAGCTGCAG	GACAATTACT	CCAAAATTGG	ACTAGCTTGC	180
TTCTCAAAGA	CGGATGAGGA	TTTCTGGGAC	TCCACTGATG	GAGAGATCTT	GAACAGACCC	240
TGCTTGCAGG	TTAAGAGGCA	ACTGTATCAG	CTCATTGAAG	A CCTC A CTTT	CACAACCOOC	
CACCACACCA	mmmcma ca cm	maga area a	CICATIGAAG	AGGIGACIII	GAGAACCTTT	300
CAGGACACCA	TTTCTACAGT	TCCAGAAAAG	CAGCTAAGTA	CTCCTCCCTT	GCCCAGAGGT	360
GGAAGACCTC	AGAAAGTGGC	AGCTCACATT	ACTGGGATCA	CTCGGAGAAG	CAACTCAGCT	420
ጥጥል ልጥጥ ሮሮል ል	TOTOTALOGA	TOOMANAGAGG	TT CCCC C	2000000000	CANCICAGCI	•
TIMITICCAA	ICICCAAGGA	IGGAAAGACC	TTAGGCCAGA	AGATTGAATC	CTGGGAGTCC	480
TCTCGGAAAG	GGCATTCATT	TCTCAACCAC	GTGCTCTTTA	GGAATGGAGA	GCTGGTCATC	540
GAGCAGGAGG	GCCTGTATTA	САТСТАТТСС	CAAACATACT	TOCOMETTO	CCAACCECAA	
C3 CCCMMCC3	3 C 3 M C C M C M C		CHACATACT	ICCGATITCA	GGAAGCTGAA	600
GACGCTTCCA	AGATGGTCTC	AAAGGACAAG	GTGAGAACCA	AACAGCTGGT	GCAGTACATC	660
TACAAGTACA	CCAGCTATCC	GGATCCCATA	GTGCTCATGA	AGAGCGCCAG	A A A C A C C C C C C C C C C C C C C C	
TOOTOONONO	A MCCCCCA CMA		GIGGICAIGA	DAJJOUGCAG	AAACAGCIGI	720
IGGICCAGAG	ATGCCGAGTA	CGGACTGTAC	TCCATCTATC	AGGGAGGATT	GTTCGAGCTA	780
AAAAAAAATG	ACAGGATTTT	TGTTTCTGTG	ACAAATGAAC	ATTTGATGGA	ССТССАТСАА	840
CAACCCACCT	TCTTTGGAGC		33Cm33		CCIGGAICAA	840
CARGCCAGCI	TCTTTGGAGC	CITTITAATT	AACTAA			876

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	720 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATGGAGCCAG GGCTGCA	ACA AGCAGGCAGC	TGTGGGGCTC	CTTCCCCTGA	СССДСССДТС	60
CAGGTGCAGC CCGGCTC	GGT AGCCAGCCC	TGGAGAAGCA	CGAGGCCCTG	GAGAAGCACA	120
AGTCGCAGCT ACTTCTAG	CCT CAGCACCACC	GCACTGGTGT	GCCTTGTTGT	GGCAGTGGCG	180
ATCATTCTGG TACTGGT	AGT CCAGAAAAAG	GACTCCACTC	CAAATACAAC	TGAGAAGGCC	240
CCCCTTAAAG GAGGAAA	TTG CTCAGAGGAT	CTCTTCTGTA	CCCTGAAAAG	TACTCCATCC	300
AAGAAGTCAT GGGCCTA	CCT CCAAGTGTCA	AAGCATCTCA	ACAATACCAA	ACTGTCATGG	360
AACGAAGATG GCACCAT	CCA CGGACTCATA	TACCAGGACG	GGAACCTGAT	AGTCCAATTC	420
CCTGGCTTGT ACTTCAT	CGT TTGCCAACTG	CAGTTCCTCG	TGCAGTGCTC	AAATCATTCT	480
GTGGACCTGA CATTGCAC	GCT CCTCATCAAT	TCCAAGATCA	AAAAGCAGAC	GTTGGTAACA	540
GTGTGTGAGT CTGGAGT	rca gagtaagaac	ATCTACCAGA	ATCTCTCTCA	GTTTTTGCTG	600
CATTACTTAC AGGTCAAC	CTC TACCATATCA	GTCAGGGTGG	ATAATTTCCA	GTATGTGGAT	660
ACAAACACTT TCCCTCTT	rga taatgtgcta	TCCGTCTTCT	TATATAGTAG	CTCAGACTGA	720

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	930 base pairs
(B)	TYPE:	nucleic acid
101	CTD ANDEDNIEGO.	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

ATGGACCAGC	ACACACTTGA	TGTGGAGGAT	ACCGCGGATG	CCAGACATCC	AGCAGGTACT	60
TCGTGCCCCT	CGGATGCGGC	GCTCCTCAGA	GATACCGGGC	TCCTCGCGGA	СССТССССТС	120
CTCTCAGATA	CTGTGCGCCC			CGGATGCTGC		•
GTTAATGTTC	GGGATCGCGA			TGAACTTCTG		180
CCAAAGCTCT	ATGGCCTAGT	СССТТТССТТ	TTGCTGCTTC	TGATCGCCGC	CHCHCHCCAC	240
ΔͲϹͲͲϹϪϹϹϹ	GCACCGACCC	TOCCITION	CECTOCITC	TGATCGCCGC	CTGTGTTCCT	300
ACCORDANCE	GCACCGAGCC	TCGGCCAGCG	CTCACAATCA	CCACCTCGCC	CAACCTGGGT	360
ACCCGAGAGA	ATAATGCAGA	CCAGGTCACC	CCTGTTTCCC	ACATTGGCTG	CCCCAACACT	420
ACACAACAGG	GCTCTCCTGT	GTTCGCCAAG	CTACTGGCTA	AAAACCAAGC	ATCGTTGTGC	480
AATACAACTC	TGAACTGGCA	CAGCCAAGAT	GGAGCTGGGA	GCTCATACCT	ATCTCA ACCT	
CTGAGGTACG	AAGAAGACAA	AAAGGAGTTG	GTGGTACACA	GTCCCGGGCT	ATCTCAAGGT	540
ጥጥጥጥር C እ እ C	TCAACCTCAC	TOROUNDITO	GIGGIAGACA	GTCCCGGGCT	CTACTACGTA	600
TTTTTGGAAC	IGAAGCTCAG	TCCAACATTC	ACAAACACAG	GCCACAAGGT	GCAGGGCTGG	660
GTCTCTCTTG	TTTTGCAAGC	AAAGCCTCAG	GTAGATGACT	TTGACAACTT	GGCCCTGACA	720
GTGGAACTGT	TCCCTTGCTC	CATGGAGAAC	AAGTTAGTGG	ACCGTTCCTG	GAGTCAACTG	. – •
			GTGGGTCTGA			780
CAGGATGCAT					GCATGGAGCC	840
		GGAGCTGTCT	TATCCCAACA	CCACCAGCTT	TGGACTCTTT	900
CTTGTGAAAC	CCGACAACCC	ATGGGAATGA				930